M.musculus

A707390 Sequence ABD057272 Gene enco ABD057272 Gene enco ABD057273 Gene enco CS125905 Sequence CS126190 Sequence A726190 Sequence A72610 Mouse mRNA AF466698 Mus muscu AR0310 Sequence AR55969 Sequence AR55969 Sequence AR55969 Sequence A7138 Sequence A708054 Sequence A7138 Sequ

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Glaichenhaus, N. and Malherbe, L.
Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses
Patent: WO 0109194-A 1 08-FEB-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers

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AX080953 Sequence
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                GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                            frame_plus_p2n model
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BD137962 1446 bp DNA linear PAT 18-SEP-2002
Nonovalent MHC-binding domain fused proteins and conjugates,
polyvalent MHC-binding domain fused proteins and conjugates,
polymer MHC-binding domain fused proteins and conjugates, and
utilization therefor.

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PRESIDENT AND FELLOWS OF HARVARD COLLEGE
OS Artificial Sequence
PN JP 200250442-A/7
PD 12-FEB-2002
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Flt-3 ligand-encoding polynucleotide as a polynucleotide-based
vaccine enhancer
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 19-FEB-1999 JP 2000532537
19-FEB-1998 US 60/075351
KAI W WUCHERPFENNIG, JACK L STROMINGER
C12N15/09, A61K35/14, A61K47/48, C07K14/705, C07K16/00, C07K19/00,
C12Q1/02;
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...or feature (16) ...(158)
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Tocation/Qualifiers (1437) ...(1446)
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Amol type="genomic DNA"
Ab_xref="taxon:32630"
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Patent: WO 0109303-A 3 08-FEB-2001;
VICAL INCORPORATED (US)
Location/Qualifiers
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                     CAGAGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGG
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Patent: WO 2004091655-A 1 28-OCT-2004;
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unclassified sequences.

1 (Dases 1 to 1581)
Boulain,J. and Ducancel,F.
BOULDIAIN,J. and DUCANDLESS, THEIR PROCESS OF PREPARATION, AND THEIR
APPLICATIONS AS AN AGENT IN DIAGNOSTIC AND IN THE THERAPEUTIC FIELD
OR AS A REAGENT RELEVANT IN MEDICAL APPROACHES
PATENT: EP 0556111-A 1 18-AUG-1993;
COMMISSARIAT ENERGIE ATOMIQUE (FR)
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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immunoglobulin; immunoglobulin gamma-2a; immunoglobulin heavy
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Unpublished
Unpublished
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Unpublished
Unbulsed (1581)
Ucancel, F.F.D.
Direct Submission
Submitted (09-FBB-1993) F.F.D. Ducancel, C.E.A, de Saclay, 91191 Gif Yvette, Cedex, FRANCE
Location/Qualifiers
1. organisme"Mus musculus"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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916 374

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474

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PAT 27-AUG-2002

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Synthetic construct
Synthetic construct
other sequences; artificial sequences.

1 (bases 1 to 1570)
Ckawa, H., Nakata, M. and Yuasa, Y.
Gene encoding antimalathion monoclonal antibody
AL Patent: JP 2001275682-A, 9 09-0CT-2001;
KANKYO MENEKT GIJUTSU KENKYUSYO KK
PN JP 2001275682-A/9
PP 31-MAR-2000 JP 200098323
PI HIDEO OKAWA, MASANOBU NAKATA, YOJIRO YUASA
PC CIZNIS/09, COTKIE/44, CIZNI/15, CIZNI/19, CIZNI/21, CIZNI/10, CI2P21/PC
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C12N5/00
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Gene encoding antimalathion monoclonal antibody.
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Beavers, L.S., Bumol, T.F., Gadski, R.A. and Weigel, B.J.
Novel recombinant and chimeric antibodies directed against a human adenocarcinoma antigen
Patent: EP 0338767-A2 4 25-OCT-1989;
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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Nishi, K., Imajuku, Y., Nakata, M., Ohde, K., Miyake, S., Morimune, K., Kawata, M. and Ohkawa, H.
Direct Submission

Direct Submission

Direct Submission

Submitted (11-DEC-2002) Kosuke Nishi, Kobe University, Research
Center for Environmental Genomics; 1-1 Rokkodai-cho, Nada-ku, Kobe, Hyogo 657-6501, Japan (B-mail:nishikosuke@yahoo.co.jp,
Tel:81-78-801-5863, Fax:81-78-871-3617)

Location/Qualifiers

1. 1570

/organism="Mus musculus"
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                                                                                                                                                                                                              1334 GGAAAAGAAGAACTGGGTGGAAAGAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCT 1393
1154 TCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTT 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nishi, K., Imajuku, Y., Nakata, M., Ohde, K., Miyake, S., Morimune, K., Kawata, M. and Ohkawa, H. Molecular characteristics of the monoclonal and recombinant antibodies specific to the insecticide malathion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                         1274 GAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTGAGGGT
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                                   eMetProGluAspileTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLy
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/cell type="hybridoma"
/note="anti-malathion monoclonal antibody MLT2-23"
                                                                                                                                                                                                                                                'note="MLT2-23 heavy chain"
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/db_xref="taxon:10090"
/clone="pG208"
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                                                                                                                         GlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArg 103
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Conservative:
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                  BARGGludspTyrAsnSerThrLeudrgValValSerAlaLeuProIleGlnHisGlnHs
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                                                       -----GAGCCCAGAGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nogoa antibodies for the treatment of alzheimer disease Nogoa antibodies for the treatment of alzheimer disease Patent: WO 2005061545-A 49 07-JUL-2005; Glaxo Group Limited (GB)
Location/Qualifiers
1. 1407
/organism="Mus musculus"
//orjanism="mus musculus"
//orjanism="musculus"
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//orjanism="musculus"
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/product="immunoglobulin gamma-2a heavy chain"
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/note="Balb/c heavy chain variable domain"
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171. .200
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417. .449
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|standard_name="framework region 3"
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/note="Balb/c IgG2a CH2 domain"
1119. .1439
/note="Balb/c IgG2a CH3 domain"
1443. .1570
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/note="Balb/c IgG2a hinge"
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GGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGT
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                                                                                                                                                                                                                                                                                                                                                           rAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGl
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Patent: WO 2005061544-A 49 07-JUL-2005;
Glaxo Group Limited (GB)
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Sequence 49 from Patent W02005061544.
CS126190.1 GI:71059163
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1. 1407
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1320.00
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REFERENCE
AUTHORS
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                                                                                                                                                                      LysHisAsnLeuGlyIleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAla 113
                                                                                                                                                                                                                                                            ProGlnAlaThrValPheProLysSerProVal ------LeuLeuGlyGlnProAsn 130
                                                                                                                                                                                                                                                                                                                ThrieulleCysPheValAspAsnIlePheProProValIleAsnIleThrTrpLeuArg 150
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AACTCTGGATCCCTGTCCAGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGAC--- 588
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                                                                  AAA-----ACAACAGCC 423
                                                                                                                                                    GluPheGlyGlnLeuIleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGlu 93
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                                                 48 -----GlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAspLys
                                                                                                                              AGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGGTCTATTATTGT
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                                                                                                     LysLysThrValTrpArgLeuPro---------
ValTyrGlnSerProGlyAsp----
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                                                                                           1143 gercacrcricaccrccacacacacrricarecricaadeacarraacercaeacac
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    1401
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/db_xref="taxon:10090"

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FVNNVEWTHAQTQTTHREDYNSTLRVVSALPICHQDDMNSGKEFKCKVNNKDLPAPIERT
ISKPKGSVRAPQVYVLPPPFEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKN
TEPVLDSDGSVFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK"
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//gene="IGHG2A"
//product="immunoglobulin heavy chain constant region gamma
2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="immunoglobulin heavy chain constant region gamma
             MMU294738 990 bp mRNA linear ROD 09-PEB-2001
Mus musculus partial mRNA for immunoglobulin heavy chain constant
                                                                    AJ294738.1 GI:12055401
Constant region; gamma 2a; IGHG2A gene; immunoglobulin heavy chain.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-SEP-2000) McLean G.R., Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 LeuGlyGlnProAsnThrieuIleCysPheValAspAsnIlePheProProValIleAsn 145
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                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                             McLean,G.R., Nakouzi,A., Casadevall,A. and Green,N.S.
Human and murine immunoglobulin expression vector cassettes
Mol. Immunol. 37 (14), 837-845 (2000)
11257305
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SOURCE
ORGANISM
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AUTHORS
TITLE
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                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                             1 (bases 1 to 1095)
Sikorav,J.L., Auffray,C. and Rougeon,F.
Structure of the constant and 3' untranslated regions of Balb/c gamma 2a heavy chain messenger RNA
Nucleic Acids Res. 8 (14), 3143-3155 (1980)
/ DNA; gamma-immunoglobulin; immunoglobulin. (house mouse)
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Matches:
Conservative:
Mismatches:
Indels:

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ROD 17-NOV-2004

1095 bp mRNA linear Mouse mRNA for gamma-2a-immunoglobulin heavy-chain. V00798.1 GI:51835

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Direct Submission
Submission
Submitted (GB-JAN-2002) Institute of Zoology, Academia Sinica, 128
Academia Road, NanKang, Taipei 11529, Taiwan, ROC
Location/Qualiffers
1. 1407
/organism="Mus musculus"
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/strain="BALB/c"
/db_xrefe"taxon:10090"
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Mus musculus strain BALB/c immunoglobulin heavy chain mRNA, partial
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                                                                                                                                             yProSerValPhellePheProProLyslleLysAspValLeuMetileSerLeuSerPr 305
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 1407)
Lai, X. S., John, J.A.C., Guo, I.C., Chen, S.C., Fang, K. and Chang, C.Y.
In vitro efficiency of intra- and extracellular immunization with
mouse anti-YGNNV antibody against yellow grouper nervous necrosis
                                                                                                                                                                                                                                                                     2 (bases 1 to 1407)
Lai, Y.-S., John, C., Guo, I.-C., Chen, S.-C., Fang, K. and Chang, C.-Y.
                                                                                                                                                                                                                                                                                                                                       480 GTTTGTGAACAACGTGGAAGTACACACAGGCTCAGACACAAACCCATAGAGAGGATTACAA
                                                                                                                                                                                                                                                                                                                                                                                             600 GGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCCGGCGCCCATCGAGAGAACATTC
  PPheValdenAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAs
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                                                              gGlyProThr1leLysProCysProProCysLysCysProAlaProAsnLeuLeuGlyGl
                                                                                                                                                                         ACCATCCGTCTTCCATCCTCCAAAGATCAAGGATGTACTCATGATCTCCTGAGCCC
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Adw71834 Murine OK
Adg12637 Monoclona
Adg1263 Chimeric
Adn97544 Artificia
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Aa22272 Mouse Zal
Aa235704 Human gly
              A044282 DR2 IGG f
Abi99027 IAS MBP 1
Abi99031 MBP 90-10
Abi99029 IAS MBP 9-10
Abi99032 MBP 1-14
Adi30316 Mbristron
Adi77690 Monoclona
Aq48037 Monoclona
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding a fusion protein comprising an alpha chain of MHC.
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ADD15694
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AA01263
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AA054652
AAW91659
ADW97544
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(CNRS) CNRS CENT NAT RECH SCI.

Glaichenhaus N, Malherbe L;

WPI; 2001-182944/18. P-PSDB; AAB67480. New soluble recombinant protein, useful e.g. as immunostimulant, comprises dimeric major histocompatibility complex molecule fused to immunoglobulin Fc region.

Example 1; Page 31-33; 43pp; French.

The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the Fc region of an immunoglobulin. The recombinant proteins, when linked to an antigenite peptide, are used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Ag-reactive T cells from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising an alpha chain of MHC molecules

Sequence 1484 BP; 414 A; 394 C; 362 G; 314 T; 0 U; 0 Other;

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1.06e-218 2655.00 100.0% 100.0% 5		1484	494	0	0	0	0
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10-048-116B-2 (1-495) x AAF55098 (1-1484)

1	MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu	20
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21		40
61	TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTAT	120
41		09
121	CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTCTTAT	180
61		80
181	GTGGACTTGGATAAGAAAACTGTCTGGAGGTTCCTGAGTTTGGCCAATTGATACTC	240
81		100
241	TTTGAGCCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAAACACAACTTGGGAATCTTG	300
101		120
301	ACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC	360
121	LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe	140
361	AAGTCCCCTGTGCTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACACATCTTC	420
141	ProProvalileAsnileThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr	160
421	CCACCTGTGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTC	480

ne 180 	ro 200	1x 220 3A 660	1u 240	la 260	 780	ro 280 	at 300	320	AT 960	18 340 AT 1020	3p 360	le 380	TC 1140	ro 400 	he 420	vs 440] AG 1320	al 460	rĠ 1380	eu 480 G 1440			
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GluthrserPheLeuValAanArgAapHisSerPheHisLysLeuSerTyrLeuThrPhe 	dapardiletyzardcyrlyrvaldi 	201 ValleulysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGly 220	rThrThrAlaProSerAlaGlnLeuGl1	JACIACAGCICCAICAGCICAGCICGA GlnLeuGluTrpGluLeuGlnAlaLe	ACAGCTGGAATGGGAGTTGCAAGCACTV	JArgGlyProThrIleLyBProCyBPr 	VG1VProSerVa1PheIlePheProPrint[rProllevalThrCysvalvalValAg	cccaracrcarerererecreereav	rTrpPheValAsnasnvalGluvalH1. 		J.veG]nPbelveCvsliveValAgnAg		eSeriys ProlysglySerValArgal :TCAAAACCCAAAGGGTCAGTAAGAGC	JGluMetThrLysLysGlnValThrLe	NGAGAIGACIAAGAAACAGGICACICI OIleTyrValGluTrpThrAenAenGl	CATTTACGTGGAGTGGACCAACAACGG	oValLeuAspSerAspGlySerTyrPh	Agrecresacrersarssrrerractr	ntipvalgluargabinsertyrsercy. 	######################################	CACAATCACCACGACTAGAGCTTCTCCCGGACTCC	CDNA; 1676 BP.
GluThrSerPhe	11eProSerAss 	ValleuLysHie 	GlyGlyGlySez	GGI GGAGGAICU Lyngluaenale	AAGGAAAATGCA	AlaSerGluPro 	ABnLeuteuGly	IleSerLeuSer	Arcrecerdade	ValGlnIleSer 	ArgGluAspTy1	Trawatsarch	TGGATGAGTGG	GluargThrIle	ProProGluGlu	CCACCAGAAGAA MetProGluAgg	ATGCCTGAAGAC	AenThrGluPro	AACACTGAACC	Glulyslysäsr Gaaagaagaa	HisAsnHisHis	CACAATCACCAC	standard; c[
161	181	201	221	241	721	261	281	301	106	321	341	361	1081	381	401	1201	1261	441	1321	461	481	1441	LT 2 19041 ABI99041
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25-FEB-2002 (first entry)

Murine pCB223 coding sequence.

Mouse, MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidiabetic; antiinflammatory; antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis; mysathenia gravis; pernicious anaemia; autoimmune encephalomyelitis; rheumatoid arthritis; systemic lupus erythematosus; ss.

Mus sp.
Synthetic.

WO200170245-Al.

27-SEP-2001.

22-MAR-2000; 2000US-0191274P.

15-MAY-2000; 2000US-0264003P.

(CORI-) CORIXA CORP.

Carter D, Zhu S, Arimilli S, Wang A;

WPF; 2001-616371/71.
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Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alphal and betal domain linked through amino acid linker and multimerization domain. Disclosure; Page 115; 147pp; English.

The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, aeach comprising an alphal domain and a betal domain linked through an anito acid linker and a multimerisation domain. The first and the second molecule are linked through the multimerisation domain to form a multimeric complex, The complex, is useful for treating autoimmune diseases. It is useful for treating sullin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (BAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention

Sequence 1676 BP; 438 A; 470 C; 407 G; 361 T; 0 U; 0 Other;

	1676	432	13	39	64	2
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-10-048-116B-2 (1-495) x ABI99041 (1-1676)

24	96	4	156
7 LeulleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeuCysGlyGlyGlu 24	37 CTCCTCTCGGCTGCTGGTGGTGGTGGTGCTGAĠCAGCCCAGGGACTGAGGGCGĀĀ 96	25 AspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyrGlnSerProGly 44	97 GACGACATTGAGGCCGACCACGTAGGCGTCTATGGTACAACTGTATATCAGTCTCCTGGA 156

45 AspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAsp 64

1042 Grerrearcricecreceaagareaagargracreargarereceergageeeeraage 1101 1102 ACATGTGTGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGATCAGCTGGTTTGTG 1161 AACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACT 1221 307 347 204 TrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGlyGlyGlySer 224 TGGGAACCTGAGATTCCAGCCCCCATGTCAGAA--------GGATCTGCCAAA 681 ThrileLysProCysProProCysLysCysProAlsProAsnLeuLeuGlyGlyProSer 287 327 367 AAGAAGGAGACTATCTGGATGCTTCCTGAGTTTGGCCAATTGACAAGCTTTGACCCCCAA 276 104 124 AATTCCACCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCCAAGTCCCCTGTG 396 144 CTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTCCCTCCTGTGATC 456 164 516 LeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAsp 184 576 ACAACAGCCCCATCGGTCTATCCACTGGCCCCTGTGTGGAGATACAACTGGCTCCTCG 741 GTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGGAAC 801 ------AlaGluLysGluLeuGluLysGluLeuGluLysGluLeuGluLeuGluLeuGluLeuGluLeuGlu 861 238 AlaLeuGluLysGlu-----AsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLys 255 ------GluProArgGlyPro 267 981 84 LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIle AsnilethripleukrgaanserlysservalthraspGlyvalfyrGluthrserPhe AspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProValLeuLysHis CTTGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTCATCCTTCTGAC GlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArgSer ThrThrAlaProSer------LeudrgvalvalSerAlaLeuDroIleGlnHieGlnAspTrpMetSerGlyLyeGluPhe LystysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeuPheGluProGln AsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProVal 288 ValPhellePheProProLyslleLysAspValLeuMetIleSerLeuSerProlleVal ThrCygValValValAspValSerGluAspAspProAspValGlnIleSerTrpPheVal AsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThr GluLeuAlaGlnAlaAlaSer--------1162 217 277 397 457 637 682 742 256 982 65 82 105 337 145 517 185 577 205 225 230 268 308 328 348 125 165 229 ò 유 δ g ઠે ద 셤 ઠે g ઠે 중 음 요 ò 셤 ò 요 ઠે 셤 ઠે ద ઠે 셤 ઠે 셤 Š ያ ያ ద ઠે 셤 ઠે ద ઠે

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                                                    CTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTC
                                                                                                         LysGlySerValArgAlaProGlnValTyrValLeuProProGluGluGluMetThr
                                                                                                                                  AAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAAGATGACT
                                                                                                                                                                               LysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAspIleTyrVal
                                                                                                                                                                                                    GluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Major histocompatibility complex class II; MHC class II; human; fusion protein; HLA-DR2; DRA*0101; binding domain; Fos; dimerisation domain; IgG; allergy; autoimmune disease; vaccine; multiple sclerosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerPheSerArgThrProGlyLys 495
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(first entry)
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Mus musculus.
Chimeric.
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17-AUG-1998
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This nucleotide sequences codes for a bivalent DR2 fusion protein obtained by fusion of the Fc portion of 1gG2a to the 3' end of a DR-alpha -Fos cDNA construct (see AAV16866). The Fc portion was amplified by RT-

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tissue
on 17-OCT
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PCR from mouse hybridoma L243. The PCR product was then fused in frame with the DR-alpha-Fos construct by overlapping PCR. The DR2-IgG fusion was expressed in the Drosophila Schneider cell system. The invention relates to new soluble monovalent and multivalent Class II MHC fusion proteins comprising a MHC Class II binding domain and a dimerisation domain or an immunoglobulin region that can be used for the treatment of allergic and autoimmune diseases (e.g. multiple sclerosis), for tolerising a subject to foreign tissue before or after organ or tissue transplantation, or for vaccination against pathogens. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                          T; 0 U; 0 Other;
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364
32
7
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                           356 G; 301
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                                                                                                                                                           8.16e-156
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83.2%
76.5%
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Best Local Similarity:
                                                                                                                            Sequence 1446
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Pred. No.:
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This nucleotide sequence codes for a divalent HLA-DR2 WHC binding domain fusion protein (see AAY31654) comprising an alpha-mating factor secretion signal, the extracellular domain of the HLA-DR2 alpha chain (see Idea in Strate) to DRA+0101), a 7-amino acid linker, the 40-amino acid leucine zipper dimerization domain of Fos, and the FC portion of IgG2a. The DR-alpha-FC chain corresponds to an antibody heavy chain. The invention provides new monovalent, multivalent and multimaric MHC Class II binding domain fusion proteins and conjugates comprising at least a binding domain of an MHC class II alpha or beta chain and a dimerization domain, especially a Fos or Jun leucine zipper domain. The MHC fusion proteins and conjugates can be used: for detecting and isolating T cells having a defined MHC/peptide complex (claimed); to stimulate or activate T cells reactive to a defined MHC/peptide complex (claimed); to stimulate or activate T cells reactive to a defined MHC/peptide complex (claimed); to treat allergic and autoimmune diseases, e.g. multiple sclerosis, rheumatoid architis, pemphigus vulgaris, and systemic lupus erythematosus; and to prevent organ or tissue transplant rejection. The DR2-IGG design was chosen to increase the affector domain, the FC region of IgG2a.

Complement fixation may result in the lysis of target T cells following complex therefore be useful for the selective depletion of autoaggressive T
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                                                                                                                                                                                                                                                                                                                                                                                        New HMC Class II binding domain fusion proteins and conjugates - used for, e.g. treating allergic and autoimmune diseases or detecting, isolating, activating or killing specific T cells.
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Matches:
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                                      "DR2-Fos-Fc"
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DB:
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                                                                                                                      300 MetileSerLeuSerProileValThrCysValValValAspValSerGluAspAspPro 319
  GCAGCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCA 789
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                                                                       790 CCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAGATCAAGATGTACTC
                                                                                                                                                320 AspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThr
                                                                                                                                                                                                                              360 AspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaPro
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/note= "alpha-mating factor secretion signal"
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1. .1440
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                                                                PheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProValLeu 125
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                    LeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIleAsn
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459
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440 LybabithrGluprovalleuabpSerabpGlySerTyrPheMetTyrSerLyBLeuarg
                                              GTGGAAAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGT
                                    ValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValH1sGluGly
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/*tag= a

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97WO-US014503.
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P-PSDB; ADW44283.
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Chimeric.
Unidentified.
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15-AUG-1997;
19-FEB-1998;
12-FEB-1999;
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Novel class II major histocompatibility complex (MHC) fusion protein having MHC class II binding domain of MHC class II alpha chain, and dimerization domain, useful for treating pemphigus vulgaris, rheumatoid arthritis.

Example; SEQ ID NO 11; 55pp; English.

systemic The present invention relates to the class II major histocompatibility complex (MHC) fusion protein having MHC class II binding domain of MHC class II alpha chain and a dimerization domain. The invention is useful in adoptive immunotherapy and tolerizing against foreign tissue. The invention is also useful for treating autoimmune diseases such as pemphigus vulgaris, rheumatoid arthritis, multiple sclerosis and systemilupus erythematosus. The present sequence is the DR2-IgG fusion protein encoding

G; 301 T; 0 U; 0 Other; Sequence 1446 BP; 414 A; 375 C; 356

Length: 1446 Macches: 364 Conservative: 32 Mismatches: 7 Gaps: 4	26 ABDILEGLUALBARDHIBVALGLYPheTyrGlYThrThrValTyrGlnSerProGlyAsp 45 ::: ::: ::: 13 GAGATCAAAGAACAAGTGATCATCCAGGCCGAGTTCTATCTGAATCCTGACCAA 69 46 IleGlyGlnTyrThrHiBGluPheAspGlyAspGluLeuPheTyrValAspLeuAspLy8 65 1 :::::: : :::: : ::: : : :::	66 LysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeuPheGluProGlnGly 85	TATACTCCGATCACCAATGTACCTCCAGAGGTAACTGTGCTCACGAACAGCCCTGTGGAA 309 LeuGlyGlnProAsnThrLeuIleCy8PheValAspAsnIlePheProProValIleAsn 145 Liillii	166 ValAsnargasphisSerPheHisIvgLeuSerTyrLeuThrPheIleProSerAspAsp 185	206 GlubrogluileProAlaProMetSerGluLeuThrGluThrGlyGlyGlyGlySer 224
ignment Scores: 3d. No.: 194.50 Aach ccent Similarity: 31.2\$ Conse st Local Similarity: 72.3\$ Indel : 10-048-116B-2 (1-495) x ADW44282 (1-1446)	26 AspileGlualaAspHisValGlyP ::: ::: ::: 13 GAGATCAAAGAAGAACATGTGA 46 IleGlyGlnTyrThrHisGluPheA 70 TCAGGCGAGTTTATGTTTGACTTTG	66 LysLysThrValTrpArgLeuProG ::		166 ValAsnArgAspHisSerPheHisI	206 GluProGluIleProAlaProMets ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::

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LysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeu---AlaGln 259
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                  MetileSerLeuSerProlleValThrCysValValValAgpValSerGluAspAspPro
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                                                                   GCAGCATCTGAGCCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCA
                                                                                                       ProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeu
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                                                                                                                                                                                                                                                              The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class Inmolecule and a second recombinant single chain MHC class II molecule, each comprising an alphal domain and a betal domain linked through an amino acid linker and a multimerisation domain. The first and the second multimeric complex, The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anemia, autoimmune encephalomyelitis (EAB), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention
                                                                                                                                                                                     Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alphal and betal domain linked through amino acid linker and multimerization domain.
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15-MAY-2000; 2000US-0204249P.
23-JAN-2001; 2001US-0264003P.
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                                                                                                                                                 Accricarccricigacgargararriargacriccaaggricaggeriggecricgecricgag 1305
                                                                                                                                                                                                                                                                                                 ASCCGAGGGGGGGAAGCGGGGGGGGGGGGGCAAAACGACACCCCCATCTGTCTATCCA 1389
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                                                              ProlleGluArgThrileSerLysProLysGlySerValArgAlaProGlnValTyrVal
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                                                                                                                                                                                                                               GAGCCGGTTCTGAACACTGG------
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1324 AGCGGAGGGGGGAAGCGGGGGGAAGCTTAGCCAAAACGACACCCCCATCTGTCTAT 1383
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                                                                                    39 ValtyrglnSerProGlyAsplleGlyGlnTyrThrHisGluPheAspGlyAspGluLeu
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                                                                                                                                                                                              820 GTATATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGATGG
                                                                                                                                                                                                                                                                                                                                  79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly
                                                                                                                                                                                                                                                                                                                                                            940 ACAAGCTTTGACCCCCCAAGGTGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                         99 IleLeuThriysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 GluProArg---GlyProThrileLysPro-------CysProProCysLysCys
                                                                                                                                                                                                                                           59 PhelyrvalAspleuAsplyslyslysThrvalTrpArgleuProGluPheGlyGlnLeu
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                                                        GlyGly------GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThr
              US-10-048-116B-2 (1-495) x ABI99033 (1-2343)
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                     2221 AATGTGCAGAAGAGCAACGAGGAAATACTTTCACCTGCTCTGTGTTACATGAG 2280
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459 ArgvalGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGlu
                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidiabetic; antiinflammatory; antiansemic; antirheumatoid; antiarchritic; neuroprotective; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis; myasthenia gravis; pernicidus anaemia; autoimmune encephalomyelitis; rheumatoid.arthritis; systemic lupus erythematosus; ss.
                                                                                                            2281 GGCCTGCACCACCATACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA 2331
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                          MBP 90-101 CH1.H.CH2.CH3 coding sequence.
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                                                                                                                                                                                                                        ABI99033 standard; cDNA; 2343
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1737.50
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65.3%
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15-MAY-2000; 2000US-0204249P.
23-JAN-2001; 2001US-0264003P.
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P-PSDB; ABB56463.
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Synthetic.
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298 ValLeuMetIleSerLeuSerProIleValThrCysValValValAspValSerGluAsp 317

ery Match:

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The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alphal domain and a betal domain linked through an amino acid linker and a multimerisation domain. The first and the second molecule are linked through the multimeriation domain to form a multimeric complex, The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune erocphalomyelities (EARS), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention
                                             Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alphal and betal domain linked through amino acid linker and multimerization domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          940 ACAAGCTTTGACCCCCCAAGGTGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    760 GGCGCTTCCTCGAGTGAAGACGACATTGAGGCCGACCACGTAGGCGTCTATGGTACAACT
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                                                                                                                                                                                                                                                                                                                                                                Sequence 2053 BP; 492 A; 585 C; 563 G; 413 T; 0 U; 0 Other;
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Matches:
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                                                                                                               Disclosure, Page 93; 147pp; English
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72.0%
69.2%
57.2%
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WPI; 2001-616371/
P-PSDB; ABB56459
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MBP 1-14 CH1.H.CH2 coding sequence
ABI99032 standard; cDNA; 2059
                                                                             (first entry)
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                                        ABI99032;
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Mouse; MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidiabetic; antilnflammatory; antiannemic; antirheumatoid; antiarthritic; neuroprofective; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis; myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis; rheumatoid arthritis; systemic lupus erythematosus; ss.

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159 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 178
                                                                                                                                                                                            Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alphal and betal domain linked through amino acid linker and multimerization domain.
                                                                                                                                                                                                                                                                            The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alphal domain and a betal domain linked through an amino acid linker and multimerisation domain. The first and the second molecule are linked through the multimerisation domain. The first and the second multimeric complex, The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune erocephalomyelitis (EAB), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention
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                                                                                          ACCTTCATCCCTTCTGACGATGATATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAG
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TGGATTGGGGAAATCAATCATGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGA 1492
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1553 GCCGCGGACACGGCTGTGTATTACTGTGCGAGAGTTATTACTAGGGCGAGTCCTGGCACA 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ımmunogenic compositions comprising Flt-3 ligand encoding polynucleotide
and one or more antigen, or cytokine encoding polynucleotides, useful for
suppressing tumor growth and for treating autoimmune diseases (e.g.
rheumatoid arthritis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of patient-specific bicistronic chimeric idiotype VR1642 (plasmid VAXID), which is used to treat B-cell lymphoma patients. The plasmid includes the cytomegalovirus immediate-early promoter, enhancer and 5' untranslated sequences, driving the expression of mouse-human chimeric immunoglobulin light and heavy chain sequences. The human light and heavy chain variable regions are derived from B-cell lymphoma cell line RAMOS. The transcriptional terminator region includes polyA and termination signals from the bovine growth hormone gene. According to the invention, co-administration of VR1642 with a plasmid (see AAR30314) encoding human Fms-like tyrosine kinase (Flt-3 ligand) provides a means of treating a patient with B-cell lymphoma. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 GlyvalLeuAlaLeuAsnThrMetLeuSerLeu---CysGlyGlyGluAspAspIleGlu
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Matches:
Conservative:
Mismatches:
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               Cytomegalovirus
Mus musculus.
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                                                                                 1721 ACAAGTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTG 1780
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1781 ACCTTGACCTGG-----AACTCTGGATCCCTGTCCAGTGGTGTGCACATCCCAGCT 1834
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                                                                                                             125 LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIle 144
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GlnasnilealaalagluLysHisAsnLeuGlyIleLeuThrLysArgSerAsnPheThr 107
                                                                                                                                                                                                                           LeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAsp 184
                                                                                                                                                                                                                                                                                                                                                                                                   rThrThrAlaProSerAlaGlnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAl 244
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                 GACGGG------AGGTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACG
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                                                                                                                                                                    145 AsnileThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPhe
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                                                     108 ProAlaThrAsnGluAlaProGlnAlaThrValPheProLy8SerProVal
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The present sequence is that of the cloning cassette of a tri-cistronic mAb17-1A expression and dihydrofolate reductase selection construct for use in the production of recombinant 1962a mAb17-1A antibody. In examples from the invention, comparison of the original, hybridoma-derived immunisation antigen 17-1A and recombinantly expressed mAb17-1A from CHO cimmunisation antigen not immunological differences in rhesus monkey critals. Both formulations showed identical kinetics building up the immunisation antigen and target antigen specific immune response, and raised 190 and 190 titres were similar. Recombinant mAb17-1A is an comparison of primates and comprising at least a part of a murine conformant antibody of the invention designed for immunisation of primates and comprising at least a part of a murine 1922 subtype amino acid sequence with mammalian glycosylation.

Recombinant DNA methods are used to produce the immunogenic antibody in a standardised manner. The humoral immune response induced by the 1962a immunogenic antibodies of the invention is significantly improved in the specificity against selected targets and epitopes. The improved
                                                                                                                                                                                        CTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGCTCCACAGGGTCTGCACAATCACCA 2625
                                                2565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; IgG2a; antibody; monoclonal antibody; mAb17-1A; cancer; vaccine;
nTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisHi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody mAb17-1A expression construct.
                                                                                                                                                                                                                                                                                                                                                         CACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 2659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "mAb17-1A kappa chain"
                                                                                                                                                                                                                                                                                     sThrihrlysSerPheSerArgThrProGlyLys 495
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25. .756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADT77690 standard; DNA; 3973
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P-PSDB; ADT77691, ADT77692.
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immune response is dependent on the glycosylation pattern of the antibody. Recombinant antibody expressed in hamster or human cells were shown to have a similar immunogenicity as antibody expressed by murine hybridoma cells. This is of particular relevance for antibodies that are to be used for immunisation purposes. The antibody may have a murine amino acid sequence or any other mammalian amino acid sequence that is combined with the murine igg2a part. Preferably mammalian sequences are human, humanized, human/murine chimeric or murine sequences. The antibody may also be an anti-idiotypic antibody or a mimotopic Abl antibody. The IgG2a immunogenic recombinant antibody or a mimotopic Abl antibody. The IgG2a immunogenic antibody. The vaccines may be used for the prophylaxis and therapy of cancer associated diseases, e.g. metastatic disease in cancer patients. The vaccine specifically modulates antigen-presenting calls in vivo or ex vivo, thus generating an immune response to the epitope that is targeted by the IgG2a immunogenic antibody. The preferred method of producing the antibody-expression construct containing at least a nucleotide sequence encoding a kappa light chain and a nucleotide sequence encoding a gamma heavy chain, where at least one of these sequence comprises a nucleotide sequence encoding at least a part of a mutine appressing the sequences under the control of a single CMV promoter to produce an intact antibody. The kappa light chain and gamma heavy contentrations of 5.100 und/ml are expressed in a shoule equance. concentrations of 5-300 ug/ml are achieved

Sequence 3973 BP; 1052 A; 1038 C; 993 G; 888 T; 0 U; 2 Other;

	60	75	1746	107	124	144	164	184
	euPheTyr PACTGACT	TGACTCT	lyglyLeu sacrcrG	snPheThr	TGGAGAT	rovallle ::: \GCCAGTG	nrSerPhe rcccAGCT	roSerAsp
	AspGluLe	ACATCTG	ProGlnG] GGCCAAGC	ArgSerA	Proval	PheProPi TTCCCTGA	TyrgluTh ::: CACACCT	PhelleP
3973 281 26 71 95	eAspGly	coGluPhe	uPheGlu ::: TTACTGG	uThrLys	OLYBSer ::: !ACTGGCC	pasnile GGGTTAT	pglyval greerere	rrbeuThr ::: }-CTCAGT
φ	HisGluPh ::: GAGAAGTT	ArgleuPr ::: cagcrcaG	LeulleLe rGGTTTGC	GlyileLe	ValPhePx ::: GTCTATCC	PhevalAe crGGTCAA	ValThrAe ::::: CTGTCCAG	LeuserTy cTCAGCAG
Length: Matches: Conservati Mismatches Indels: Gaps:	42 SerproglyaspileglyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60 :::	61 ValaspieuaspiysiysiysiysThrValTrpargleuProGluPhe75	76	88 GlnAsnileAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArgSerAsnPheThr 	108 ProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProVal 124	125 LeuleuGlyGlnProAsnThrLeulleCysPheValAspAsnIlePheProProVallle 114	145 ABNIJEThrītpleudrgABRSerLy8SerValThrAspGlyValTyrGluThrSerPhe 164	LeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAsp 184 :::::
(i. No.: 1328.50 March cent similarity: 59.5\$ Conse natch: 1328.50 March cent similarity: 59.5\$ Misma natch: 13 March 1495) x ADT77690 (1-3973)	31yG1 3GTACTAA	LysLysTh AGCACTGC	SCAAGAGA	SlutysHi	AlaProGl	AsnThrLe 3TGACTCT	Argasnse	HisserPh
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AspaspileTyrAspCysLysValGluHis-TrpGlyLeuGluGluProValLeuLysHi 204

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anti-snake small neurotoxin antibody; heavy chain; 19G2; immunoglobulin; bispecific bivalent antibody; cell-targetting; cytotoxic agent; ss.
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neurotoxin monoclonal antibody M(alpha)2-3 now monocloxin monoclonal antibody M(alpha)2-3 now monoclonal antibody M(alpha)2-3 now monoclonal antibody M(alpha)2-3 now monoclonal antibody M(alpha)2-3 now AAQ48040 no aderived cDNA using primers AAQ48041 and AAQ48042. The two amplified from the same vector, the H-chain fragment was inserted into the same vector; the H-chain fragment was inserted into the first formal and antibodian and the L-chain fragment was inserted into a cassette which contained and the L-chain fragment was inserted into a cassette which contained sequence, a signal peptide and the first formal and the transcription termination sequence of phoA. The termination codon and the transcription termination sequence of phoA. The fusion construct is expected to to encode a hybrid protein comprising two identical Ab-derived units. The invention also covers hybrid proteins containing two different Ab-derived units (i.e. to produce bispecific antibodies). When a toxic protein is used in place of phoA, the hybrid molecules can be used as cell-targetting therapeutic agents. (Updated on 15-MAR-2003 to correct New immunoglobulin hybrid proteins - with immunoglobulin fragments linked to dimeric protein, for diagnostic or therapeutic use. A fragment of the heavy chain (VH + CH1) from the anti-snake small Example 1, Fig 3A; 37pp; French

Sequence 1581 BP; 435 A; 448 C; 373 G; 325 T; 0 U; 0 Other;

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	4.24e-104	1324.50	65.4	59.04	
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ò	34	PheTyrGlyThrThrValTyrGlnSerProGlyAsp11eGly	lnSerProGlyAsp		2
g	211	TACTATATAAACTGGGTGAAGG	AGAAGCCTGGACAGGG		270
රි සි	48	TATCCTGCAAGCGGTAATACT	InTyrThrHisGluPhe 	1PheTyr ATTGACT	330
} &	61	ValAspLeuAspLysLysLys1	hrValTrpArgLeu	ě	75
q	331		::: cctacatgcagctcagc	5	
ò	76	GlyGlnLeulleLeuPheGluE	roGlnglyglyLeuGlr	60	95
qq	391	GCTGT-CTATTTCTGTGCAAGA		GGCTAC	431
ò	96	AsnLeuGlyIleLeuThrLys?	rg-SerAsnPheThrPr	_	115
qa	432	ACTITIGGACTACTGGGCCCAAGGCACCACTCTCACAGTCTCCTCACGCCAAAACAAGG		O	491
& ∴	115	nAlaThrValPheProLysSer	Proval		132
q	492	CCCATCGGTCTATCCACTGGCC	CCTGTGTGGGAGATAC	CCCATCGGTCTATCCACTGGCCCCCTGTGTGTGAGATACAACTGGCTCCTCGGTGACTCT	551
ð	132	ulleCysPheValAspAsnilePheProProValileAsnileThrTrpLeuArgAsnS	PheProProValileAs		152
q	552	Aggardccrgdrcaagggrra	Trectranscration	- Act	505
č	152	rLysSerValThrAspGlyValTyrGluThrSerPheLeuValAsnArgAspHi	TyrGluThrSerPheLe	sSerPh	172
qq	909	TGGATCCCTGTCCAGTGGTGTC	CACACCTTCCCAGCTG	rcctgcagtctgacct	559
δ	172	eHisLysLeuSerTyrLeuThrPhe	IleProSerA	IleTyrAspCysLysVa	192
qq	099	CTACACCCTCAGCAG-CTCAGT		GACTGTAACCT	691
č	192	1GluHis-TrpGlyLeuGluGluProV	аlьечьувні	roGlulleProAlaP	212
qa	692	CGAGCACCTGG		- O	103
È	212	roMetSerGluLeuThrGluTh	rGlyGlyGlyGlyser1		232
q	704	CCAGCCAGTCCATCACC	TGCAATGTGGCC	CCAGCCAGTCCATCACCTGCAATGTGGCCCACCCGGCAAGCAGGACAAGG	754
ò	232	euGluLygGluLeuGlnAlaLe	euGluLysGluAsnAlaC		252
q	755	- 1			89.
č	252	laLeuGluLysGluLeuAlaGl	aGlnAlaAlaSerGluProA	erGluProArgGlyProThrlleLyBProC	272
qq	769		COST CONTRACTOR CONTRA	-	962
ò	272	ysProProCysLysCysProAl	aProAsnLeuLeuGlyC	ysProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheP	292
q	797	GTCCTCCATGCCAAATGCCCAGG	Accreaccrerreger		956
ò	292	roProLyslleLysAspValLe	wMetlleSerLeuSer	roProLysileLysAspValLeuMetileSerLeuSerProlleValThrCysValValV	312
q	857	CTCCAAAGATCAAGGATGTACT	CATGATCTCCCTGAGCC		916
કે ક	312	alAspValSerGluAspAspPr	OABDValGlnIleSer/	alkspvalserGlukspkspyerokspyalGlnileSerTrpPheValksnksnvalGluv : 	332
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                       GTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCA 1096
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prion disease; 44BlH; ds; therapeutic; monoclonal antibody; heavy chain.
                                                                                                                                                                                                                                                                          ACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTGTATGGTTCTT
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Umetani A;
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The invention describes an agent (1) for treating prion disease or delivering a substance to the lesioned region of prion disease, comprishing a mesenchymal cell. Also described are: a nucleic acid (II) having an anti-prion antibody gene comprising: an antibody heavy chain gene having SEQ ID No: 1, 3, 5, 30, 32 and 34, a nucleotide sequence consisting of a degenerate genetic code, which encodes a polypeptide same

Claim 4; SEQ ID NO 5; 34pp; Japanese.

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cc as that of the above nucleotide sequence, a nucleotide sequence, which is a mutant of the above sequences or a nucleotide sequence that is complementary to the above sequences and that hybridizes under stringent conditions with the above sequences and that hybridizes under stringent conditions with the above sequences; and an antibody light chain gene having SEQ ID No: 2, 4, 6, 31, 33 and 35, a nucleotide sequence conditions with the above nucleotide sequence a nucleotide sequence that is a mutant of the above sequences, or a nucleotide sequence, which is a mutant of the above sequences, or a nucleotide sequence that is conditions with the above sequences and that hybridizes under stringent conditions with the above sequences and that hybridizes under stringent conditions with the above sequences and that hybridizes under stringent conditions with the above sequences and that hybridizes under stringent conditions of interprion chimeric antibody (IV) comprising variable region of antibody encoded by (II) and constant region of antibody of animal other than constant prion proliferation inhibition activity, comprising transducing a gene that provides abnormal prion proliferation inhibition activity to constant antibody being obtainable by (MI) or by utilizing (II) or (III); a cutilized for treating prion disease; use of a mesenchymal cell for cutilized for treating prion disease; use of a mesenchymal cell for preparing or prion disease, comprising utilizing mesenchymal cell. (I) is useful for treating prion disease or delivering a substance to the lesioned region of prion disease, comprising utilizing mesenchymal cell. (I) is useful for having abnormal prion proliferation inhibition activity. (I) or (VI) is useful for treating prion disease. (II) or (III) or (III) or having abnormal prion proliferation disease. This sequence an anti-Promise of menoclonal antibody heavy chain. Note: This sequence and anti-Promise of prion disease. The symptome of prion disease. The symptome of sequence of the prince of prion or 
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1039 GTTTGTGAACAACGTGGAAGTACACACACACTCAGACACAAACCCATAGAGAGTTACAA 1098
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ВР AEB21727 standard; DNA; 1407 (first entry) 08-SEP-2005 AEB21727; 821727

Anti-Nogo-antibody 2A10 heavy chain polynucleotide.

antiparkinsonian; anticonvulsant; protein production; therapeutic; pharmaceutical; amyloidosis; metabolic disordar; cerebrovascular ischemia; cardiovascular disease; neurological disease; brain injury; injury; spinal cord injury; vulnerary; dementia; genetic disorder; Creutzfeldt Jakob disease; Huntingtons chorea; genetic disorder; Creutzfeldt Jakob disease; infection; antiinflammatory; inflammatory; inflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antibody; heavy chain; ds. neuroprotective; nootropic; cerebroprotective; vasotropic;

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The invention describes a method of modulating production of an amyloidogenic peptide comprising contacting a cell which is expressing contacting a cell which is expressing contacting accell which is expressing contacting to the precursor from which the amyloidogenic peptide is derived and a Nogo polypeptide, with a Nogo antagonist. Also described are: use of a Nogo antagonist in the manufacture of a medicament for the treatment or prophylaxis of a disease involving amyloidosis; and a method of treatment or prophylaxis of Alzheimer's disease comprising administering to the human in need an anti-Nogo antibody. The invention is used for modulating contaction of amyloidogenic peptide in, e.g. Alzheimer's disease, stroke, traumatic brain injury and spinal cord injury, fronto-temporal dementias, peripheral neuropathy, Parkinson's disease, Huntington's disease, creutzfeldt-Jakob disease, amyotropic lateral sclerosis, multiple sclerosis, or inclusion body myositis. The invention provides an unexpected route for therapeutic intervention in particularly Alzheimer's disease, this sequence represents an anti-Nogo-antibody 2AlO heavy chain Modulating production of amyloidogenic peptide in, e.g. Alzheimer's disease, by contacting cell and Nogo polypeptide with Nogo antagonist Sequence 1407 BP; 378 A; 396 C; 346 G; 287 T; 0 U; 0 Other; Example 4; SEQ ID NO 49; 53pp; English 20-DEC-2004; 2004WO-GB005343 22-DEC-2003; 2003GB-00029684. 22-DEC-2003; 2003GB-00029711. (GLAX) GLAXO GROUP LTD Prinjha RK, WPI; 2005-522181/53 Percent Similarity: Best Local Similarity: WO2005061545-A2 polynucleotide 07-JUL-2005. Alignment Scores: Hussain I,

1407 285 26 68 108 Length: Matches: Conservative: Mismatches: Indels: Gaps: 8.87e-104 1320.00 64.0% 58.6% Query Match: DB:

(1-1407)US-10-048-116B-2 (1-495) x AEB21727

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39 0	39 ValTyrGlnSerProGlyAspIleGly	47
178 G		237
48 -	48GlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAspLys 65	65
238 G	238 GGTACTAACTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTG	297
1 99	66 LystysThrValTrpArgLeuPro	73
298 A	298 AGCACAGCCTACATGCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGT 357	357
74 G	74 GluPheGlyGlnLeuIleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGlu 93	93
358 G		411
94 L	94 LysHisAsnLeuGlyIleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAla 113	113
412 AAA	 AAACAACAGCC 423	423
114 P	114 ProGlnAlaThrValPheProLysSerProValLeuLeuGlyGlnProAsn 130	130
424 C	TGGGTCTATCCACTGGCCCCTGTGTGGAGATACAACTGGCTCCTCGGTG 477	477

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rTyrserCysserValValHisGluGlyLeuHisAsnHisHisThrLysSerPheSe 490
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                                                                                       SerPheHisLysLeuSerTyrLeuThrPheIleProSerAspAspAspIleTyrAspCys 190
                                                                                                                                                                                                               LysValGluHis-TrpGlyLeuGluGluProValLeuLysHisTrpGluProGluIlePr 210
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New antibody or its functional fragment that binds with and neutralizes human neurite outgrowth useful for treating or prophylaxis of stroke and other neurological disease e.g. traumatic brain injury, spinal cord
                                                                                                                                                                                                                          disease;
                                                                                                                                            cerebroprotective, vasotropic; neuroprotective; vulnerary; nootropic antiparkinsonian; anticonvulsant; neuroleptic; antibody engineering; pharmaceutical; cerebrovascular ischemia; cardiovascular disease; neurological disease; brain injury; injury; spinal cord injury; Alzheimers disease; degeneration; dementia; neuropathy; parkinsons disease; Huntingtons chorae; genetic disorder; multiple sclerosis; immune disorder; cetuzzfeldt Jakob disease; infection; schizophrenia; psychiatric disorder; motor neurone disease; cns-gen.; muscular-gen.; ds.
                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                           Mcadam
                                                                                                                        antibody 2A10 heavy chain polynucleotide SEQ ID NO 49.
                                                                                                                                                                                                                                                                                                                                                                                                           Hussain F,
                                                                                                                                                                                                                                                                                                                                                                                                           Grundy RI,
Wilson PA;
                                                       BP
CCGGACTCCGGGTAAA 1398
                                                      DNA; 1407
                                                                                                                                                                                                                                                                                                                                20-DEC-2004; 2004WO-GB005325.
                                                                                                                                                                                                                                                                                                                                                    22-DEC-2003; 2003GB-00029684 22-DEC-2003; 2003GB-00029711
                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           Ellis JH, Eon-Duval A,
Plumpton C, Prinjha RK,
                                                                                                                                                                                                                                                                                                                                                                                      (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-479448/48
                                                       AEB08761 standard;
                                                                                                                                                                                                                                                                                   WO2005061544-A2
                                                                                                    08-SEP-2005
                                                                                                                                                                                                                                                            Unidentified
           1383
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Example 3; SEQ ID NO 49; 143pp; English.

injury, Alzheimer's disease.

The invention describes an antibody (A1) or its functional fragment, that chinds with and neutralizes human neurite outgrowth (NOGO). Also described are: providing a first vector encoding a heavy chain of the antibody; corrected antibody and providing a second vector encoding a light chain of the antibody; corresponding the host cell in culture media (preferably serum free) under conditions permissive to the secretion of the antibody from the host cell into the culture media; recovering (and optionally purifying) the into the culture media; recovering axonal sprouting involving contacting a human axon with an anti-NOGO antibody. The antibody is useful in the preparation of a medicament for treating or prophylaxis of stroke and correct injury, Alzheimer's disease, frontotemporal dementias (tauopathies), cord injury, Alzheimer's disease, frontotemporal dementias (tauopathies), cord injury, Parkinson's disease (Huntington's disease and multiple sclerosis); Creutzfeldt-jakob disease (CDD), Schizophrenia, amyotrophic lateral sclerosis (ALS), inclusion body myositis. The contingual diseases/disorder tine a human patient suffering, or at risk of developing, stroke or other contaction polynucleotide used in the creation of recombinant anti-NOGO arribodies. antibodies.

Sequence 1407 BP; 378 A; 396 C; 346 G; 287 T; 0 U; 0 Other;

Aliqnment Scores:

rArgThrProGlyLys 495

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290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 aglnLeuGluLysGluLeuGlnAlaLeuGluLysGluAsnAlaGlnLeuGluTrpGluLe 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 LysHisAsnLeuGlyIleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAla 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 AAA-----ACAACAGCC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 ProGlnAlaThrvalPheProLysSerProVal-----LeuLeuGlyGlnProAsn 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 ThrieulleCysPheValAspAsnIlePheProProValIleAsnIleThrTrpLeuArg 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||||| ||||::::: |||||||:::
532 AACTCTGGATCCCTGTCCAGTGTGCACCTTCCCAGCTGTGTCCTGAGTCTGAC--- 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 SerPheHisLysLeuSerTyrLeuThrPheIleProSerAspAspAspIleTyrAspCys 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::: |||||| ||||| 589 ---CTCTACACCCTCAGCAG-CTCAGT------GACTGT 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 LysvalGluHis-TrpGlyLeuGluGluProValLeuLysHisTrpGluProGluIlePr 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 oAlaProMetSerGluLeuThrGluThrGlyGlyGlySerThrThrAlaProSerAl 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 681 CAAGGTGGACAAGAAATT----- 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GAGCCCAGAGGCCCACATCAA 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           783 CTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGT 842
                                                                                                                                                                                                                                    178 GTGAAGCAGAGGCCTGGACAAGGCCTTGAGTGGATTGGAAATATTAATCCTAGCAATGGT 237
                                                                                                                                                                                                                                                                         48 -----GlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAspLys 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluPheGlyGlnLeurleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGlu 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 uGlnAlaLeuGluLysGluLeuAlaGlnAlaAlaSerGluProArgGlyProThrIleLy
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                                                                                                                                                                                          39 ValTyrGlnSerProGlyAsp------IleGly-----
  1407
285
26
68
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13
  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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È	330	1GluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgVa	350
op Q	903	GGAAGTACACACAGCTCAGACACAAACCCATAGAGAGATTACAACAGTACTCTCCGGGT	962
ò	350	1ValSerAlaLeuProIleGlnHigGlnAapTrpMetSerGlyLygGluPheLygCygLy	370
qq	963	GGTCAGTGCCCTCCCCATCCAGCACCAGGATGAGTGGCAAGGAGTTCAAATGCAA	1022
ò	370	8ValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySe	390
Dp	1023	GGTCAACAACAAAGACCTCCCAGCGCCCCATCGAGAACCCATCTCCAAAACCCAAAGGGTC	1082
ò	390	rValArgAlaProGlnValTyrValLeuProProProGluGluGluMetThrLy8Ly8Gl	410
QQ	1083	AGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAAGATGACTAAGAAACA	1142
È	410	nValThrLeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpTh	430
qq	1143	GGTCACTCTGACTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGAC	1202
ò	430	rAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGl	450
QQ	1203	CAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGGAACCAGTCCTGGACTCCTGATGG	1262
È	450	YSerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSe	470
qq	1263	TTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAATAG	1322
ò	470	TTyrSerCysSerValValHisGluGlyLeuHisAsnHisHisHisThrLysSerPheSe	490
q	1323	CTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTC	1382
ò	490	rArgThrProGlyLy8 495	
ор	1383	CCGGACTCCGGGTAAA 1398	

Search completed: May 31, 2006, 23:18:22 Job time : 1013.56 secs



cDNA enco Murine pC Sequence

Mouse MHC Alphalalp IAB alpha Murine pC CDNA enco

Aat60698 Aaq35054 Abi99044 P

uence:

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AAT 60700 CDNA enco AAT 17588 Vector SC AAT 60704 MOUSE WHC AAT 60701 ALPHAIALD AAT 60702 IAS MBP 1-14 AAD 99027 IAS MBP 1-14 AAD 99031 MBP 1-14 AAD 99030 IAS MBP 9 AAD 9900 IAS MBP 9 IAS MBP 9
                               Adx26089 Novel cel
Aat66285 Lab-alph
Aa56919 Mouse I-A
Aat17587 Vector SC
Aax86988 SCTI sing
Aax8069 Single ch
Aca60743 Mouse MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin; major histocompatibility complex; Fc region; antigen; T lymphocyte; immunostimulant; vaccine; infection; tumour; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a fusion protein comprising an alpha chain of MHC.
                                ADX26089
AAT06285
AAQ56919
AAT17587
AAT86988
                                                                                                                   AATG0698
ABD35054
ABD350044
AATG0700
AATG0700
AATG0704
AATG0704
AATG0704
AATG0704
AATG0987
AATG0903
                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ74306
ADV43942
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AEB23393
AAI58351
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1. .1482
/*tag= a
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                                                                    WO200109194-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999;
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           Aaf55098 DNA encod
Adg31223 Class II
Aav12067 Murine IA
                                                                               May 31, 2006, 22:51:28 ; Search time 557.439 Seconds (without alignments) 5215.692 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1496
1 MPCSRALILGVLALNTMLSL......QAASEPRGPTIKPCPPCKCP 278
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           GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                       using frame_plus_p2n model
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                                                                                    WPI; 2001-182944/18.
P-PSDB; AAB67480.
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ដ New soluble recombinant protein, useful e.g. as immunostimulant, comprises dimeric major histocompatibility complex molecule fused immunoglobulin Fc region.

Example 1; Page 31-33; 43pp; French

The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the Fc region of an immunoglobulin. The recombinant proteins, when linked to an antigenic peptide, are used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Ag-reactive T cells from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising an alpha chain of MHC molecules

Sequence 1484 BP; 414 A; 394 C; 362 G; 314 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
Indels:
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Local Similarity:
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61 TGCGGAGGTGAAGAGGCTTTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AAGTCCCCTGTGCTGCTGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC 420
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                                                                                                                                                                                                                                                                                                    41 GINSexProGlyAspileGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr
                                                                                                                                                                                                                                                                                                                                                                         61 ValkapLeukapLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu
                                                                                                                                                            MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu
1484
278
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Peptide-class II major histocompatibility complex (MHC) composite, useful for detecting antigen specific CD4+ T-cell, comprises antigen peptide containing epitope of mucous membrane invasive protein, and extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel class II major histocompatibility complex (MHC) antigenic peptide composite comprising a peptide containing the T-cell antigenic determinant of a mucous membrane invasive protein and the extracellular region of a class II MHC molecule or at least part of the extracellular region of the class II MHC molecule having an amino acid sequence comprising one or more deletions, substitutions or
                                                                                                                                                             200
                                                                                                                                                                                                                                              600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    class II major histocompatibility complex; MHC; CD4+ T-cell detection; flow cytometry; mucous membrane invasive antigen; I-Ab(alpha)-leucine zipper fusion; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluThrSexPheLeuValAgnArgAgpHisSexPheHisLysLeuSexTyrLeuThrPhe
                                                                                                                                                                 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro
                                                                                                                                                                                                        ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysGluAsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLysGluLeuAlaGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaSerGluProArgGlyProThrIleLyBProCyBProProCyBLyBCyBPro 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .777
A-tag= a / A-facture | Company | Compa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class II MHC-related I-Ab(alpha)-leucine zipper (LZ) fusion cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ř
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 8; 30pp; Japanese.
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additions. The molecule of the invention may be useful for detecting an antigen-papecific CD4+ T-cell by flow cytometry and for presenting a microorganism-derived mucous membrane invasive protein as an antigen. The method of the invention enables efficient detection of antigen-specific activation of CD4+ T-cells in the amotous membrane. The current sequence is that of the class II major histocompatibility complex-related I-AD(alpha)-leucine zipper (LZ) fusion cDNA of the invention.

Sequence 777 BP; 193 A; 207 C; 195 G; 182 T; 0 U; 0 Other;

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180
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                                                                                                                                                                                                                                                                                                              61 TGTGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           658 CCGCGCGGATCCACTACAGCTCCATCAGCTCGAAAAAAGAGCTCCAGGCCCTGCAG 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601 Grichgaaacachddaachchdadariccadccccardrichca---Gcagaccregrr 657
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                                                                                                                                                                                                                              GlnSerProGlyAspileGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr
                                                                                                                                                                                                                                                                                                                                                                                                121 CAGTCTCCTGGAGACATTGGCCAGTACACATTTGAATTTGATGGTGATGAGTTGTTCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe
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                                                                                                                                                                                                         MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu
                                                                                                                                                                                                                                                                                       21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr
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                    777
232
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                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                  5.27e-112
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ignment Scores:
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                       No.:
                                                                                                      ary Match
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This nucleotide sequence comprises a PCR product obtained by amplification of mouse splenocyte cDNA using primers (see AAV12063 and AAV12064) designed for the amplification of Inda alpha chain full-length cDNA. IAd beta chain cDNA (see AAV12069) has been similarly obtained. The CDNA. IAd beta chain cDNA (see AAV12069) has been similarly obtained. The CDNA. IAd beta chain cDNA (see AAV12069) has been similarly obtained. The confirmation of CT and sequences were expressed at the cells. COMPLIANT (MHC) class II IAd heterodimers were expressed at the cells. The current on relates to the preparation and use of synthetic antigen conventing matrices, in particular antigen presenting colls such as insect cells that have been transfected to produce MHC antigen presenting confirmation of the matrices are used to activate naive CD4+ T cells and to shift the ongoing activation state into a preferred differentiated population of Th1 or Th2 cells. CAPICAL APPLICATIONS include the treatment of autoimmume disease, e.g. diabetes, multiple sclerosis, autoimmune thyroiditis, systemic lupus erythematosus, ather and contract conditions include the area of an asthma and contract conditions include and contract conditions and an another another and contract contract conditions include the another conditions include the another conditions and contract conditions and activate and contract conditions and co
                                                                                                                                                                                                           Major histocompatibility class II antigen; MHC class II; T cell; T lymphocyte; Th1; Th2; activation; CD4+; antigen presenting cell; APC; autoimmune disease; diabetes; multiple sclerosis; autoimmune thyroiditis; systemic lupus erythromatosus; mysathenia gravis; Crohn's disease; inflammatory bowel disease; allergy; asthma; contact sensitivity; immunotherapy; therapy; IAd alpha chain; mouse; ds; circular; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic antigen presenting cell for activating CD4+ T cells - usefutreat autoimmune disease, e.g. diabetes, multiple sclerosis, Crohn's disease and inflammatory bowel disease, or allergy, e.g. asthma and contact sensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4713 BP, 1211 A, 1166 C, 1152 G, 1184 T, 0 U, 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peterson PA;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 92-94; 141pp; English.
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                         BB
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                      CDNA; 4713
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                                                                                                                                                                   Murine IAd alpha chain cDNA.
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                         AAV12067 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAY-1996;
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                                                                   AAV12067;
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Sheppard PO;

Deshpande S,

Gross JA,

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The present sequence encodes a novel soluble fused major histocompatibility complex (MHC) heterodimer:peptide complex, comprising thistocompatibility complex (MHC) heterodimer:peptide complex, comprising septide able to associate with a peptide binding groove of the MHC molecule, linked in frame to the 2nd domain by a 5-25 residue linker and a DNA encoding a 3rd MHC domain linked in frame to the DNA encoding the antendence peptide by a DNA encoding a 5-25 residue linker. The complex can be used to induce immunological tolerance in adults susceptible to, or suffering from an autoantigen related disease, e.g. insulin dependent class and antigen presenting cells, to induce anergy (immunological noncresponding antigen are permanently linked into a single chain, corresponding antigen are permanently linked into a single chain, obviating the requirement for complex heterodimer fruncation or formation, the complex eliminates inefficient and non-specific peptide loading. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProValileAsnileThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGlu 161
                                                                                                                                                        Novel fused major histocompatibility complex:antigenic peptide complex - useful to induce tolerance to an autoantigen-related disease e.g. insulin -dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlubroGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThr 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysArgSerAsnPheThrProAlaThrAsnGluAlaProGluAlaThrValPheProLys 121
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                                                                                                                                                                                                                         Example 3; Page 129-132; 142pp; English.
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1105.00
100.0%
100.0%
73.9%
95US-0005964P.
                                                                               Kindsvogel W, Reich EP,
                              (ZYMO ) ZYMOGENETICS INC (ANER-) ANERGEN INC.
                                                                                                              WPI; 1997-052337/05.
P-PSDB; AAW10513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 27-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                          LysSerProValLeuteuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | IleProSexhspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluThrSerPheLeuValAgnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
                                   638
                                                                                                                                                                                                               PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLyBHisAsnLeuGlyIleLeu 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soluble, fusion; major histocompatibility complex; MHC; heterodimer; complex; antigen; binding groove; tolerance; autoantigen; disease; insulin dependent; diabetes mellitus; IDDM; antagonist; T cell; anergy; presenting cell; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
                                                                                                                                              ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeulleLeu
                                                                                                                                                                    GTGGACTIGGATAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTC
                                                                                                                                                                                                                                   CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyxGlyThrThrValTyr
                                                                               GlnSerProGlyAspileGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr
                                                                                                              579 cadricriceradacarricaccadracacardaarrrraargargargargrrerar
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95US-00482133.
95US-00483241.
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mat_peptide
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07-JUN-1995;
07-JUN-1995;
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12-SEP-1997
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1344 203 0 0 0

Length: Matches: Conservative: Mismatches:

Indels:

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                                                                                                                                                                                            ACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTCATC
                                                                                           ProSerAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProVal
ThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIle
                                                                                                                                             cerrerandardacarrinandacrecaadgredacacarregedecredadgecegrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse, MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidiabetic; antidiflammatory; antiansemic; antiarheritic; neuroproecetive; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis; myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis; rheumatoid arthritis; systemic lupus erythematosus; ss.
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15-MAY-2000; 2000US-0204249P.
23-JAN-2001; 2001US-0264003P.
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P-PSDB; ABB56471.
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Synthetic.
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                                               808
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396 144 456

AsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProVal 124

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277 GGGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGAATCTTGACTAAGGAGGTCA

217 AAGAAGGAGACTATCTGGATGCTTCCTGAGTTTGGCCAATTGACAAGCTTTGACCCCAA 85 GlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArgSer

104

AspaspileGlualaaspHisValGlyPheTyrGlyThrThrValTyrGlnSerProGly

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LysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeuPheGluProGln

AspileGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeuAsp

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LeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeuCysGly-----GlyGlu

US-10-048-116B-2_COPY_1_278 (1-278) x ABI99041 (1-1676)

1676 215 13 39 64

Length:
Matches:
Conservative:
Mismatches:
Indels:

2.34e-98 1083.00 68.9% 65.0%

Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores: Pred. No.:

Score:

AsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPhe 164

AACATCACATGGCTCAGAAATAGTAAGTCAGTCACAGACGGCGTTTATGAGACCAGCTTC

457

145

LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIle

397 CTGCTGGGTCAGCCCAACACCCTCATCTGCACAACAACATCTTCGCTCCTGTGATC

184

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CTIGICAACCGIGACCATICCTICCACAAGCIGICTIAICTICACCTICATCCTTCTTCAACCGTGACCTTCTGAC 576
                                                  204
                                                               ------AlaGluLysGluLeuGluLysGluLeuGluLysGluLeuGln 237
                                                                                                                                                                                                                                                                             802 TCTGGATCCCTGTCCAGTGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTAC 861
                                                                                                                                                                                                                                                                                                                  238 AlaLeuGluLysGlu-----AsnAlaGlnLeuGluTrpGluLeuGlnAlaLeuGluLys 255
                                                                                                                                                                                                                                                                                                                                  267
                                                                                                     IrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGlyGlyGlyGlySer 224
LeuValabadrgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAsp
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Sequence 1676 BP; 438 A; 470 C; 407 G; 361 T; 0 U; 0 Other;

molecule of the invention

The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MIC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alphai domain and a betal domain linked through an amino acid linker and a multimerisation domain. The first and the second molecule are linked through the multimerisation domain. The first and the second multimeric complex, The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent disbetes, multiple eclerosis, myssthenia gravis, pernicious ansemia, autoimmune encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus erythematogus. The present sequence encodes a single chain MHC class II

Disclosure; Page 115; 147pp; English

AAQ03169;

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ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
                                                                                                                                                                                                                                                                                                                                                                                 LysserProvalLeuLeuGlyGlnProAsnThrLeuIleCysPhevalAspAsnIlePhe 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 ileProSerAspAsplleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValleulvehistrpGlubroGlulleProAlaProMetSerGluLeuThrGluThr 219
6 ATGCCGCGCAGCAGCAGCTCTGAGGGGTCCTCGCCCTGACCACCATGCTCAGCCTC
                                                                                                                                                                          61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu
                                                                                                                                                                                                                                                                                                                                      366 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysGlyGlyGlydaspAspIleGlwAlaAspHisValGlyPheTyrGlyThrThrValTyr
                                                                                                     41 GlnSerProGlyAsp11eGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr
                                                                                                                                                                                                                                           PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLy8HisAsnLeuGlyIleLeu
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                                                                                                                                                                                                                                                                                                                                  1-A (Class II) histocompatibility protein;
major histocompatibility complex antigen; MHC-II; acetylcholine receptor;
myasthenia gravis; autoantigen; autommune disease; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New complexes of histo-compatible glyco.protein - with antigenic peptide(s) and label or toxin, used to target antigen specific T helper cells.
         922 AATGTGGCCCACCCGGCAAGCAGCACCAAGGTGGACAAGAAAATTGAGCCCAGAGGGCCC
                                                                                                                                                                                                                                                                                     Class II major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 776 BP; 177 A; 205 C; 199 G; 195 T; 0 U; 0 Other;
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Mismatches:
Indels:
                                                                            982 acaarcaagcccrgrccrccargcaaargccca 1014
                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                     Sequence encoding the I-Ab-alpha chain of histocompatibility complex (MHC) antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BR;
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                                                                                                                                                  BP
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89US-00367751.
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94.1%
91.8%
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                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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21-JUN-1989;
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31-OCT-2002
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425

485

365

100

80

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Novel cell pain response detection method-related mouse gene SeqID435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pain; animal disease model; expression; analgesic; antiaddictive; nootropic; anticonvulsant; vasotropic; neuroprotective; tranquilizer; antischmeute; antiarthitic; osteopathic; opthalmological; antiinflammatory; antipruritic; dermatological; antiulcer; gastrointestinal-Gen.; nephrotropic; gymecological; hepatocropic; antiparkinsonian; neuropetic; laxative; gene therapy; neuropathic pain; Alzheimers disease; Parkinsons disease; motor neurone disease; Huntingtons disease; schizophrenia; gene; ds.
                                                                                                                ВР
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                                                                                                                ADX26089 standard; DNA; 978
                                                                                                                                                                                                                                                                                                                                          (first entry)
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RESULT 7
ADX26089
ID ADX26089
XX
AC ADX2
XX
DDT 05-M
XX
DDT 05-M
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M anti
XM Anti
XM
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0-048-116B-2_COPY_1_278 (1-278) x AAQ03169 (1-776)

: y Match:

Local

: No ::

Lavery DJ; Chiang LW, Χu Υ, J1 R, WPI; 2005-163258/17 Tong J, Jin G,

Detecting pain responses in a cell, useful in identifying potential therapeutic and diagnostic candidates for treating pain, by identifying genes that are differentially expressed in a model of neuropathic pain.

Example 1; SEQ ID NO 435; 173pp; English.

This invention relates to a novel method of detecting a pain response in a cell which comparises determining the expression level in a test cell of at levels in an animal model of pain, where similar or identical expression levels in an animal model of pain, where similar or identical expression levels indicate a pain response in the test cell. The invention may be useful for the development of compounds with an analgesic, antiaddictive, noncropic, antionical managesic, antiaddictive, noncropic, antionical managesic, antiaddictive, noncropic, antionical managesic, antiantal managesic, operationic similar antionical, antiinflammaticy, antiprutific, dermatclogical, antiinflammaticy, antipruticic, dermatclogical, antiinflammatcy, antipruticic, dermatch activity whilst therapeutic and diagnostic candidates for treating pain, including agonists and antagonists for the gene or gene products as potential uneuropathic pain, nociceptive pain, chonical pain, including alsociated with rheumatic disease, and disociated with cancer, anxiety, depression, headache, asthma, rheumatic disease, and disociated with cancer, anxiety, depression, headache, asthma, rheumatic disease, decorbing a struction of presumed esophageal crisis, retinopathy, inflammatory eye disorders, pruritus, ulcer, inflammatory bowel disease, inflammatory bowel disease, inflammatory explain, functional disease, described and disease, described bladder disorder, inflammatory bowel disease, inflammatory inflammatory explain, functional disease, described bladder disorder, inflammatory bowel with demonstrated become and disease, and diseas analysed in the method of

Sequence 978 BP; 218 A; 263 C; 247 G; 250 T; 0 U; 0 Other;

978 203	2100 4
Length: Matches:	Conservative: Mismatches: Indels: Gaps:
7.05e-98 1075.00	93.64 92.74 71.98 14
lignment Scores:	<pre>ccent Similarity: s: Local Similarity: ery Match: :</pre>

-10-048-116B-2_COPY_1_278 (1-278) x ADX26089 (1-978)

- 24 Ariecciscocascadadecrerisarrerisassicoceresecenes caracteres de as a Ariecciscocas de Ariecciscoca de Ariecciscocas de Ari 1 MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAsnThrMetLeuSerLeu
- 21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr
- 9 41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr
- - ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu 80 5

101 Thrive 	-DEC-1990; 90US-00655840 -APR-1991; 91US-00690840 NER-) ANERGEN INC. larma SD, Lerch BL, Clark '1; 1993-036056/04.	tr 1993-U30U30/U1 tre major MHC-pep sponse such as a sclosure; Fig 8; sequence (AAT062
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GlnSerProGlyAsp1leGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | IleProSerhapAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
                                                                                                                                                                                                                                                                               141 ProProValileAsnileThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHC; major histocompatibility complex; toxic conjugate; autoimmunity; autoimmune disease; helper T-cell; T-lymphocyte; acetylcholine receptor; myelin basic protein; I-Ab; ds.
                                                                                                                                                                                                                                                                                                                                                                                                    ValAspleuAsplyslyslysThrValTrpArgleuProGluPheGlyGlnLeuIleLeu 80
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appropriate MHC molecule via the I-Ab-alpha (or -beta) chain sequence. The resulting conjugate is used in the treatment of autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValleuLysHisTrpGluProGlulleProAlaProMetSerGluLeuThrGluThr 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAACACTGGGGCCTGGAGGAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                     LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe
                                           Sequence 776 BP; 177 A; 205 C; 199 G; 194 T; 0 U; 1 Other;
                                                                                       776
200
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14
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                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1072.00
93.6%
91.3%
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(first entry)
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                                                                                                                 ent Similarity:
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08-JUL-1994
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                                                                                                                                                y Match:
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The acetylcholine receptor alpha subunit given in sequence AAR45946 (corresponding mRNA in AAQ56918) and the myelin basic protein given in AAA45947 are antigenic peptides associated with autoantigens. They have been conjugated with MHC class II components such as I-Ab- alpha chain (encoded by sequene AAQ56919) and I-Ab-beta chain, (encoded by AAQ56920) and a toxin or label to form conjugates used to target helper T-cells for the treatment of autoimmune diseases. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysserProvalLeuleuGilyGlnProAsnThrLeulleCysPheValAspAsnIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CysG1yG1yG1ydspAspI1eG1uAlaAspHisValG1yPheTyrG1yThrThrValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThriysargSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHC-mediated toxic peptide conjugates - useful for ameliorating auto-
                                                                                                                                                                                                                                                                                                                                                                            BP; 177 A; 205 C; 199 G; 194 T; 0 U; 1 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                       Disclosure; Fig 8.1-8.2; 42pp; English
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                                                                                              88US-00210594.
89US-00367751.
90US-00576084.
                                                                                                                                                                Clark
                                                                          90US-00635840
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1072.00
93.6%
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Percent Similarity:
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9
Query Match:
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Pred. No.:
                                                                          28-DEC-1990;
                                US5284935-A.
                                                                                                23-JUN-1988;
21-JUN-1989;
                                                                                                                      30-AUG-1990
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426 CCTCCTGTGTGTCAACATCACATGGCTCAGAAARAGCAAGTCAGTCGCAGACGGTGTTTAT 485
                                                                                         546 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAAACACTGGGGCCTGGAGGAGGAGGCG 605
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/label= I-Ad_alpha-TM
/label= "murine MHC class II I-Ad gene alpha-transmembrane
domain"
                                                                   161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
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/label= I-Ad_alphal
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1068. 1352
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/label= I-Ad_alpha2
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1353. .1505
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//label= I-Ad_betal
//note= "murine MHC class II I-Ad gene beta-1 domain"
453. .734
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//tabel= I-Ad_beta2
/note= "murine MHC class II I-Ad gene beta-2 domain"
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/label= OVA 323-339
/mabel= "chicken ovalbumin residues 323-339"
138. .167
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note= "10 residue linker peptide"
68. .452
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note= "24 residue peptide linker"
107. .1067
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CDS
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AAT17587 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SCT1. The MHC fusion complex comprises at least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a presenting peptide covalently linked to the MHC molecule and opt. a transmembrane domain. DNA encoding a MHC fusion complex may be cloned into a host cell to express that modulate, pref. antagonise, T cell covacionity DNA encoding a MHC fusion complex or a single chain fusion complexes may be used to vaccinate a mammal against a trajected disorder. CT the fusion complexes may be used to suppress an immune response in an animal suffering from an immune disorder e.g. multiple sclerosis, insulincedependent diabetes mellitus, rheumatoid arthritis, mysathenia gravis or chronic allergies. The complexes may also be used in the treatment of livestock and pets such as cats and dogs. The MHC fusion complexes can be produced such that they contain a single antigenic peptide including one of known structure, additionally a wide range of peptides can be presented for T cell interaction.
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                                                                                                                                                                                                                                                                                                                              Major histocompatability complex fusion complex for modulating T ceactivity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1508 BP; 337 A; 414 C; 440 G; 317 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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95US-00382454
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98.5%
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                                                                                          31-JUL-1995,
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01-FEB-1995;
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99 IleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal 118

972 ATACTCTTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAAGATTGGGA 1031

79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly

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BP
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Best Local Similarity:
Query Match:
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                                                                                                                                                        1331
                                                               1332 GAGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAA 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single chain major histocompatibility complex comprising linked alpha and beta chains - useful for suppressing an immune response to an auto: immune disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, etc.
                                                                                             178
                                                                                                                                                                             199 GluProValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGlu 218
                                                     158
                                                                                                                                    179 ThrPhelleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 198
                                                                                                                                                  1272 ACCTTCATCCCTTCTGATGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAG
                                                                                             ValTyrGluThrSerPheteuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu
                                                   139 IlePheProProVallleAsnIleThrTrpLeuArgAsnSerIysSerValThrAspGly
                                                                                                                                                                                                                                                                                                                                                               Construction; major histocompatibility complex; MHC; fusion complex; SCTI single chain gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the construction of major
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wong HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 17; Page 137-139; 217pp; English.
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6. .1508
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Σ
                                                                                                                                                                                                                                                                                  AAT86988 standard; DNA; 1508 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US001617
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                                                                                                                                                                                                                                                                                                                                                SCT1 single chain gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DADE-) DADE INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-402555/37.
P-PSDB; AAW29213.
                                                                                                                                                                                                                                          1392 ACT 1394
                                                                                                                                                                                                                      219 Thr 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-1997;
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                                                                                                                                                                                                                                                                                                                            27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | IlePheProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VallyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Major histocompatibility complex; MHC; single chain MHC; sc-MHC; Ig; peptide binding groove; immunoglobulin; T cell receptor; immune response; immune-related disorder; antigenic peptide; fusion protein; ss.
                                                                                                                                                                            851
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                                                                                                                                                                                                                                                                                    PheTyrValAspLeuAspLysLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeu
                                                                                                                                                                                                                                                                                                           ThrPheIleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCTTCATCCCTTCTGATGATGACATTATGACTGCAAGGTGGAGGCACTGGGGCCTGGAG
                                                                                                                                         GlyGly------GluAspAsplleGluAlaAspHisValGlyPheTyzGlyThzThz
|||||||
|GCGGGTTCCTCGAGTGAAGACGACTATGAGGCCGACCACGTAGGCTTCTATGGTACAACT
                                                                                                                                                                                                                                    PheFroLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn
                                                                                                                                                                                                          valtyrGinserProglyAspileGlyGlnTyrThrHisGluPheAspGlyAspGluLeu
                                                                                                                                                                                                                                                                                                                                                         | IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                              IleLeuThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single chain IAd/OVA 323-229 MHC fusion protein encoding DNA.
198
0
3
1
                                                                                                        US-10-048-116B-2_COPY_1_278 (1-278) x AAT86988 (1-1508)
 Matches:
Conservative:
Mismatches:
Indels:
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Single chain major histocompatibility complex class I complexes
                                                                                       Wong HC;
                                                                                       Jiao J,
                                                                                       Rhode PR, Acevedo J, Burkhardt M,
97US-00960190.
                                         (SUNO-) SUNOL MOLECULAR CORP.
                                                                                                                                 WPI; 1999-418411/35.
P-PSDB; AAY27111.
29-OCT-1997;
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1272 ACCTTCATCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAG 1331

179 ThrPheIleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu

ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu

159

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Example 1; Fig 1; 148pp; English.

The invention relates to new single chain major histocompatibility complex (sc-MHC) class II complexes that comprise a peptide binding groove, and a modified class II beta 2 chain or covalently linked immunoglobulin (Ig) light chain content (II) region. The MHC complexes are useful for detection and analysis of peptide ligands, pathogenic Teclis, for functional, cellular and molecular assays. They can be used to identify and isolate T cell receptor and/or MHC agonists and antagonists. They can also be used to cells involved in immune-related disorders. They can also be used to raise antibodies and to screen immune cells. It is also use in a method of suppressing an immune response in mammals. The sc-MHC complexes comprising modified class II beta 2 chains and/or Ig-c1 regions are soluble and provide enhanced yield. These MHC complexes also contain single antigent peptides readily isolated from expressing cells in significant quantities. The polyspecific MHC complexes also provide a means to detect cells expressing multiple target structures with a single complex. The present sequence represents a DNA encoding a single chain

Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

1508 1198 0 0 3	6	/alGlyPheTyrGlyThrThr 38 	31uPheAspGlyAspGluLeu 58 			3lualaProGlnalaThrVal 118 	LeuIleCysPheValAspAsn 138 	SerLysSerValThrAspGly 158
6 Length: Matches: Conservative: Mismatches: Indels: Gaps:	(1-278) x AAX89069 (1-1508)	GlyGlyGluaspaspileGlualaasphisvalGlyPhefyrGlyThrThr GGCGGTTCCTCGAGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACT	Valtyrginserproglyaspilegiydintyrthrhisglupheaspglyaspgluleu 	PheTyrValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeu 	IleleuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGly 		PheProlysSerProValLeuleuGlyGlnProAsnThrLeulleCysPheValAspAsn 	IlePheProProValIIeAshII eThrTrpLeUArgAshSerLysSerValThrAspGly
icores: 1.15e-96 1065.50 idarity: 98.5\$ Similarity: 98.5\$	278	61y61y61 GCGGTTCCTCGAGTGA	ValTyrGlnSerProGl	PheTyrValAspLeuAsj 			PheProLysSerProVa 	ePheProProvali
ignment Scores: ad. No.: 2re: crent Similarity st Local Similar ary Match:	-10-048-116B-2_COPY_1	22	39 852	59	79	1032	119	139

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1332 GAGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAA 1391
218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a major histocompatibility complex (MHC) fusion complex (I) comprising an MHC molecule that contains a peptide-binding groove, and a presenting peptide covalently (e.g. an antigenic peptide) linked to the MHC molecule, where (I) is capable of modulating the activity of a T cell. Also included are a DNA construct coding for the complex, where the MHC molecule is a class II MHC (e.g. mouse I.Ad or I-As or I human HLA-DR1 (human leukecyte antigen-DR1), a multivalent MHC fusion complex comprising two or more linked complexes, identifying a peptide that can modulate the activity of T cells (involving introducing into host cells cloning vectors that each contain the fusion complex DNA, culturing the host cells under conditions suitable for expression of the MHC fusion complex, and selecting host cells that express MHC fusion complex that modulate the activity of T cells), a single recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis,
199 GluProValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGlu
                                                                                                                                                                                                                                                                                                                       MHC; major histocompatibility complex; gene therapy; fusion complex; peptide-binding groove; T cell modulation; class II MHC; vaccine; autofiment disorder; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes mellitus; myasthenia gravis; immunogen; chronic allergy; mouse; ds; I-Ad; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edwards AC;
                                                                                                                                                                                                                                                                                         Mouse MHC I-Ad/Ova 323-339 synthetic gene SCT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grammer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 17; Fig 28; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhode PR, Weidanz JA, z P, Jiao JJJ;
                                                                                                                                                                                 ACA60743 standard; DNA; 1508 BP.
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95US-00382454.
97US-00776084.
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                                                                                                                                                                                                                                                      16-JUN-2003 (first entry)
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P-PSDB; ABU72107.
                                                                                                        1392 ACT 1394
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01-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-1997;
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Synthetic.
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                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus
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expression vector comprising DNA that codes for the alpha and beta chains of the fusion complex MMC protein, a single recombinant expression vector comprising DNA that codes for a T cell costinulatory factor and the alpha and beta chains of the MMC fusion complex. The DNA constructs can contain heterologous leader peptide sequences and Kozak sequence for efficient expression of the fusion complex. Also included are inducing an immune response in a mammal (including vaccinating a mammal against a targeted disorder, by administering DNA sequence comprising a fusion complex, or DNA sequence coding for a fusion complex which is a single chain fusion molecule) and suppressing an immune response in a mammal by administering to the mammal a DNA sequence comprising an expression vector, encoding a full length MMF molecule that contains a transmembrane domain, and a presenting peptide that is a T cell receptor (TCR) antagonist or partial agonist and is covalently linked to the MMC protein, or DNA sequence coding for the fusion complex which is a single chain fusion molecule. The methods are useful for identifying a peptide that can modulate the activity of T cells, inducing an immune response in a mammal (including vaccinating a mammal against a targeted disorder) and for suppressing an immune response in a mammal against insulin-dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or chronic allergies. The present sequence encodes a mouse MHC class II I-Ad fusion complex of the

Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;

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1272 Accricarccrircigargargacarirargaciaccaaggiggagcacriggggccriggag 1331
                                                                                                                                                                                                                                                                                                                                               1092 Treeceaagreecengreeregreagecaaceceaacecerrareregrerae 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 IlePheProProVallleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 VallyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 ThrPhelleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 GluProValLeuLy8HisTrpGluProGluIleProAlaProMetSerGluLeuThrGlu 218
                                                                                                                                                                       851
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                                                                                                                                                                                                                                                               PheTyrValAspLeuAspLysLysThrValTrpArgLeuProGluPheGlyGlnLeu 78
                                                                                                                                                                                                    39 ValTyrGlnSerProGlyAsplleGlyGlnTyrThrHisGluPheAspGlyAspGluLeu
                                                                                                                                                                                                                                                                                                                           79 IleLeuPheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLy8Hi8AsnLeuGly
                                                                                                                                        GlyGly------GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThr
                                                                                                                                                        1508
198
0
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3
                                                                                                          0-048-116B-2_COPY_1_278 (1-278) x ACA60743 (1-1508)
 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                Gaps:
1.15e-96
1065.50
98.5%
98.5%
                                 ent Similarity:
Local Similarity:
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      No.
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A novel soluble fused major histocompatibility complex (MHC)

heterodimer:peptide complex, comprises DNA encoding 1st and 2nd MHC

comains, e.g. the present sequence, linked by DNA encoding a 5-25 residue

linker, and a DNA encoding an antiquency peptide able to associate with a

complex and a DNA encoding an antiquency peptide able to associate with a

complex can be used to induce immunological tolerance in adults

complex can be used to induce immunological tolerance in adults

cusceptible to, or suffering from an autoantigen related disease, e.g.

susceptible to, or suffering from an autoantigen related disease, e.g.

insulin dependent diabetes mellitus (IDDM), by antagonising the binding

of particular T cells and antigen presenting cells, to induce anergy

(Immunological non-responsiveness) in the targeted T cell. As the

cherrodimers and corresponding antigen are permanently linked into a

single chain, obviating the requirement for complex heterodimer

cruncation or formation, the complex eliminates inefficient and non-

specific peptide loading. (Updated on 27-AUG-2003 to correct OS field.)
1332 GAGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAA 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel fused major histocompatibility complex:antigenic peptide complex - useful to induce tolerance to an autoantigen-related disease e.g. insulin-dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                             Soluble; fusion; major histocompatibility complex; MHC; region; heterodimer; complex; alpha2; antigen, binding groove; tolerance; autoantigen; disease; insulin dependent; diabetes mellitus; IDDM; antagonist; T cell; anergy; presenting cell; NOD mouse; Class II; alpha1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sheppard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 588 BP; 153 A; 153 C; 136 G; 146 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                            Alphalalpha2 region of Class II NOD mouse MHC (IAg7) cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .588
/*tag= a
                                                                                                                                                           AAT60698 standard; cDNA; 588 BP.
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95US-00482133.
95US-00483241.
95US-0005964P.
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                                                                                                                                                                                                                                 (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-052337/05.
P-PSDB; AAW10505.
                                                                                            1392 ACT 1394
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07-JUN-1995;
27-OCT-1995;
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12-SEP-1997
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                                                                                                                                          GlyaspileGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyrValAspLeu
                                                                                                                                                         61 GGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTATGTGGACTTG
                                                                                                                                                                                    84 GlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeuThrLysArg
                                                                                                                                                                                                                                          SerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerPro
                                                                                                                                                                                                                                                                                                                          301 GIGCIGCIGGGICAGCCCAACACCCTTAICTGGCTTTGIGGACAACATCTICCCACCTGIG
                                                                                                                                                                                                                                                                                                                                                         144 IleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSer
                                                                                                                                                                                                                                                                                                                                                                    361 ATCAACATCACATGGCTCAGAATAGCAAGTCAGTCACACAGACGGCGTTTATGAGACCAGC
                                                                                                                                                                                                                                                                                                                                                                                                  164 PheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspaspaspile TyraspCysLysValGluHisTrpGlyLeuGluGluProValLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGATGACATTTATGACTGCAAGGTGGACACTGGGGGCCTGGAGGAGCCGGTTCTGAAA
                                                                                                                                                                                                                                                                                           241 TCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCCAAGTCCCCT
                                                                                                   GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyrGlnSerPro
                                                                                                                   1 GAAGACGACATIGAGGCCGACCACGIAGGCTTCTAIGGIACAACTGTTTATCAGTCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                              421 TICCICGICAACCGIGACCAITCCITCCACAAGCIGICITAICTICACCIICAICCITCI
                                                                                                                                                                                                                                                                                                                124 ValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor; epitope; myasthenia gravis; MG; antigen; MHC; IAB; alpha; beta; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
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ary Match:
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binding site;
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21-MAY-1993
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The AChR peptide 195-215, which has been characterised as an epitope in myasthenia gravis (MG) in humans and in mice, may be connected to the N-terminal antigen binding site of a polypeptide derived from an MHC antigen associated with MG. For example, if the recombinant complex is to be used in mice, the AChR peptide may be incorporated into a sequence encoding either the I-Ab-alpha or I-Ab-beta chain (see AAQ35054-55 respectively). If the AChR peptide is to be incorporated into the beta chain, for example, the oligonucleotide may be inserted as a replacement for the leader sequence. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheGluProGinGlyGlyLeuGlnAsnileAlaAlaGluLysHisAsnLeuGlyIleLeu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365
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                                                                                                            - useful in treating deleterious immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ValAspLeuAspLysLysLysThrValTrpArgLeuProGluPheGlyGlnLeuIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 CAGICTCCIGGAGACAITGGCCAGIACACAITIGAAITIGAIGGIGAIGAGIGTICIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGACGCTCCTCAAGCGACTCTGTTCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 GIGGACTIGGATAAGAAGGAGACTGTCTGGATGCTTCCTGAGTTTGGCCAATGCCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGACCAGCTTCTTCGTCAACCGTGACTATTCCTTCCACAAGCTGTCTTATCTCACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 776 BP; 178 A; 211 C; 192 G; 194 T; 0 U; 1 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                    BL;
                                                                                                            Pure major MHC-peptide complex response such as auto:immunity.
                                    Lerch
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(ANER-) ANERGEN INC
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ch completed: May 31, 2006, 23:18:27 time : 562.439 secs

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                                        AX080954 Sequence
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CS121774 Sequence
CS121762 Sequence
CS121780 Sequence
CS121780 Sequence
A7021780 Sequence
A702241 Multi-fun
AX70234 Sequence
BD022360 Multi-fun
AX772537 Sequence
CQ889913 Sequence
CQ889913 Sequence
CQ889913 Sequence
CQ889913 Sequence
CQ889915 Sequence
CS125905 Sequence
CS125905 Sequence
CS125905 Sequence
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CQ806513 Sequence
AR393789 Sequence
AX084107 Sequence
AR393797 Sequence
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Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses
Patent: WO 0109194-A 1 08-FEB-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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/note="unnamed protein product; ligation de fragments
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    1484
    Acganism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"

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Sequence 1 from Patent WO0109194.
AX081280
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TITLE
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V0798 Mouse mRNA
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                        GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                          GAAAAGAAGTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTG
TGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCAGCGCCCATC
                  1081 TGGATGAGTGGCAAGGAGTTCAAATGCAAGTCAACAACAACAAGAGACCTCCCAGCGCCCATC
                                                                                                                                                                                                          ATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGGGTAAACTACAAG
                                                                  GAGAGAACCATCTCAAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCT
                                                                                      GAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCT
                                                                                                                                      CCACCAGAAGAAGAGATGACTAAGAAACAGGTCACTCGTGACCTGCATGGTCACAGACTTC
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Synthetic construct
synthetic construct
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Whocherpfennig, K.W. and Strominger, J.L.
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Antagonists 11-15
Patent: WO 2004035622-A 10 29-APR-2004;
F. HOFFMANN-LA ROCHE AG (CH)
Location/Qualifiers
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                                                                                                                                                                               Score 957.6; DB 2;
Pred. No. 1.5e-249;
0; Mismatches 234;

    .1446
    /organism="synthetic construct"
/mol_type="genomic DNA"
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Past Local Similarity 81.8%;
Autches 1136; Conservative 0
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                                                                                          CCATGCAAATGCCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCA
                                             GAAAAGGAACTGGCTCAGGCAGCATCTGAGCCCCAGAGGCCCCACAATCAAGCCCTGTCCT
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Sequence 27 from Patent WO2004035622.
CQ806532.
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Patent: WO 2004035622-A 27 29-APR-2004;
F. HOFFMANN-LA ROCHE AG (CH)
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Buthoria, Buarchontoglires; Primates; Catarrhini;
Hominidae, Homo.
                                                                                                                                                                                                                                1300 AAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTC
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                                               GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGAGGAAGTACAC
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Antagonists 11-15
Patent: WO 2004035522-A 26 29-APR-2004;
P. HOFFMANN-LA ROCHE AG (CH)
Location/Qualifiers
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Sequence 26 from Patent 1
CQ806531
CQ806531.1 GI:47111925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="immunoglobulin heavy chain constant region gamma
                  AJ294738
AJ294738.1 GI:12055401
AD2016tant region; gamma 2a; IGHG2A gene; immunoglobulin heavy chain.
Mus musculus (house mouse)
Mus musculus
                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (18-SEP-2000) McLean G.R., Cell Biology, Albert Eins
College of Medicine, 1300 Morris Park Avenue, Bronx, New York
                                                                                                                                                                                  McLean, G.R., Nakouzi, A., Casadevall, A. and Green, N.S.
Human and murine immunoglobulin expression vector cassettes
Mol. Immunol. 37 (14), 837-845 (2000)
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/function="immune response"
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1. .990
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McLean, G.R.
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                                                                                                                                                        Length 1108;
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                                                                                                                                            uery Match 47.2%; Score 701.2; DB 2; sest Local Similarity 93.3%; Pred. No. 1.38-179; atches 733; Conservative 0; Mismatches C1.

    .1108
    Organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="nucleic acid for mutated

Location/Qualifiers
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 ->990
 /gene="IGKG2A"
 /product="immunoglobulin heavy chain constant region gamma 2a" 1026 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGAT 1085 ö GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACACCTCAGACACAAACCCATAGAGA 1025 845 410 965 291 TGAGCCCAGAGGCCCACACATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 906 CCTGAGCCCCATAGTCACATGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 411 CCTGAGCCCCATAGTCACATGTGTGGTGGATGAGGATGAGCGAGGATGACCCAGATGTCCA 471 GATCAGCTGGTTTGTGAACAACGTGGAAGTACACACACAGCTCAGACCACAAACCCATAGAGA 531 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGAT GAGTGGCAAGGAGTTCAAATGCAAGTCAACAACAAGAGCCTCCCCAGCGCCCATCGAGAG 786 TGAGCCCAGAGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAGATCAAGGATGTACTCATGATCTC Gaps ö Length 990; 0; Indels Query Match 47.2%; Score 700.6; DB 6; Best Local Similarity 100.0%; Pred. No. 1.8e-179; Matches 700; Conservative 0; Mismatches 0; 1086

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MANU294738 990 bp mRNA linear ROD 09-FEB-2001 Mus musculus partial mRNA for immunoglobulin heavy chain constant

NOITINE 5ULT 6 7294738 7US

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TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAACCT 350
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                                            CTTGGGTGGACCATCCGTCTTCCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC
                                                                                                                                      CCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA
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directed against
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100.0%; Pred. No. 1.9e-179;
tive 0; Mismatches 0; Indels 0;
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1 (bases I to 1341)

1 (bases I to 1341)

Novel recombinant and chimeric antibodies adenocarcinoma antigen
Patent: EP 0338767-A2 4 25-OCT-1989;

Location/Qualifiers
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    .1341
    /organism="unknown"
    /mol_type="unassigned DNA"

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/ codon start=1
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/ product="gamma-2a immunoglobulin heavy chain"
/ protein id="CAA24178.1"
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/ db_xref="UniProtxB/Swisa-Prot:P01863"
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FVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDMSGKEFKCKVNNKDLPAPIERT
ISKRKGSVTARAQVYVLPPPEEEMTKKQYTLTCKVYDPMSGKEFKCKVNNKGLPAPIERT
ISKRKGSVTARAQVYVLPPPEEEMTKKQYTLTCKVYDPMSGKEFKCKTELNYKN
TEPVLDSDGSYFMYSKLRVEKKOMVERNSYSCSVVHEGLHNHHTTKSFSRTPGK"
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       GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCAGCGCCCATCGAGAG
                                                   AACCATCTCAAAACCCAAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC
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Mouse mRNA for gamma-2a-immunoglobulin heavy-chain.
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/mol_type="mRNA"
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Mus musculus
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea, Muridae; Murinae; Mus.
1 (bases I to 1407)
Lai, Y. S., John, J.A.C., Guo, I.C., Chen, S.C., Fang, K. and Chang, C.Y.
In vitro efficiency of intra- and extracellular immunization with
mouse anti-YGNNV antibody against yellow grouper nervous necrosis
                                                                                                                                                942 GGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGAT
                                                                                                                                                                                                                                                                                                               AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC
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                                       TGAGCCCAGAGGCCCACAATCAAGCCCTGTCCTTCCATGCAAATGCCCAGCACCTAACCT
                                                     702 TGAGCCCAGAGGCCCACAATCAAGCCTGTCCTCCATCCAAATGCCAGCAGCACCTGTAACCT
                                                                                             CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC
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  Local Similarity 100.0%; P. Conservative 0;
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AF466698.1 GI:27127159
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
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1242 GAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAA
                                                          CTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC
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M-csf-specific monoclonal antibody and uses thereof
Patent: WO 2005068503-A 1 28-JUL-2005;
CHIRON CORPORATION (US); Liu, Cheng (US)
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/mol_type="unassigned DNA"
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Lai,Y.-S., John,C., Guo,I.-C., Chen,S.-C., Fang,K. and Chang,C.-Y. Direct Submission
Submitted (108-JAN-2002) Institute of Zoology, Academia Sinica, 128
Academia Road, NanKang, Taipei 11529, Taiwan, ROC
Location/Qualifiers
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/db xref="GI: 21727144"
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VTLCCLVKGYFPEPVTLTWNSGSLSSGVHTFPRAVLQSDLYTLSSSVTVTSSTWPSGSI
TCNVAHPASSTKVDKKIEPRGPTIRPCPPCKCPAPNLLGGSPSVFIFPPKIKDVLMISL
SPITYCTVVDVBSDDDDVQISWFVNNVTVHTWAQTGTREBDYNSTIRVVSALPIOHQDW
MSGKEFKCKVNNKDLPAPIERTISRPKGSVRAPQVYVTLPPPEEEMTKKQVWTLCMYTD
FWFBDIYVEWTNNGKTELNYKNTBPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVH
EGLHNHHTTKSFSRTPGK"
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mushae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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Patent: WO 9109967-A 3 11-JUL-1991;
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                                                                                                                                                    .musculus OKT3 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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PAT 27-AUG-2002
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PD 09-0CT-2001
PF 31-MAR-2000 JP 2000098323
PI HIDEO OKAWA,MASANOBU NAKATA, YOJIRO YUASA
PC C12N15/09, C07K16/44, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/ PC
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C12NS/00
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                                                                                                                1266 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGGAGCTAAACTACAAGAACAC
                                                                                                                                      1225 TGAAGACATTTACGTGGAGTGGACCAACAACGGGAAACAGAGGTAAACTACAAGAACAC
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                                    AGAAGAAGAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC
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BD057272.1 GI:22602878
JP 2001275682-A/9.
Synthetic construct
synthetic construct
other sequences, artificial sequences.
other sequences, artificial sequences.
I (bases Ito1570)
Okawa, H. Nakata, M. and Yuasa, Y.
Gene encoding antimalathion monoclonal antibody antimalathion monoclonal antibody RANKYO MENEK GIUTTSU KENKYUSYO KK
PN JP 2001275682-A/9
PD 09-0CT-2001
PP 31-MAR-2000 JP 2000098323
PI HIDBO OKAWA, MASANOBU NAKATA, YOJIRO YUASA
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Gene encoding antimalathion monoclonal antibody,
BD057272
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1. 1570
1. 0570
1. 078anism="synthetic construct"
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                                                             1165 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACGAGACTTCATGCC 1224
                                                                                                                  TGAAGACATTTACGTGGAGTGGACCAACAACAAAAACAGAGGTAAACTACAAGAACAC 1325
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1105 AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC 1164
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                                      1206 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCC
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Unknown.
Unknown.
Unclassified.
1 (bases 1 to 1570)
1 Adair, J. Robert., Athwal, D. Singh. and Emtage, J. Spencer.
Humanised antibodies
Patent: US 5859205-A 6 12-JAN-1999;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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6 from patent US 5859205.
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Sequence (
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PAT 08-OCT-2004
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                                                    TGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCCAAATGCCCAGCACCTAACCT
                    925 GAICAGCTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAAACCCATAGAGA
                                                                                                    GAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCAGCGCCCATCGAGAG
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Jolliffe, L.K., Zivin, R.A., Adair, J.R. and Athwal, D.S. CD3 specific recombinant antibody
Patent: US 6750325-A 6 15-JUN-2004;
Celltech R&D Limited; Slough;
GBX;
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1405 TCACCACCACGACTAAGAGCTTCTCCCGGGACTCCGGGTAAA 1444
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Sequence 6 from patent US 6750325.
AR559698 GI:53969764
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                                                                               AACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACC
                                                                                                                                                AACCATCTCAAAAACCCAAAGGGTCAGTAAGAGCTCCACACGTATATGTCTTGCCTCCACC
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(Loase 1 to 1570)

Adatr,J.R., Athwal,D.S. and Emtage,J.S.

Humanized antibodies

Patent: US 6632927-A 6 14-OCT-2003;

Celltech Therapeutics Limited; Berkshire;

GBX;
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Sequence 6 from patent US 6632927.
AR409372. GI:40160268
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1. .1570
/organism="unknown"
/mol_type="mRNA"
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::ch completed: June 1, 2006, 04:11:19 : time : 8835.58 secs

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May 31, 2006, 23:41:05; Search time 1026.58 Seconds (without alignments) 10085.747 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaf55098 DNA encod	Abi99041 Murine pC	Aat99707 DR2-IgG f	Aax87813 HLA-DR2 a	Adw44282 DR2-IgG f	Ab199027 IAS MBP 1	Ab199033 MBP 90-10	Ado07566 Fusion pr	Ado07578 Fusion pr	Ado07577 Fusion pr	Adl15694 Murine im	Aec20762 M-CSF gpe	Aed19725 Anti-PrP	Adv26108 Mouse OKT	Adw71834 Murine OK	Aag12637 Monoclona	Adq91058 Murine OK	Adt77690 Monoclona
SUMMARIES	ID	AAF55098	ABI99041	AAT99707	AAX87813	ADW44282	ABI99027	ABI99033	AD007566	AD007578	AD007577	ADL15694	AEC20762	AED19725	ADV26108	ADW71834	AAQ12637	ADQ91058	ADT77690
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	& Query Match	99.9	71.9	64.5	64.5	64.5	48.9	48.7	47.2	47.2	47.2	47.2	47.2	47.2	47.2	47.2	47.2	47.2	47.2
	Score	1484	1067.4	957.6	957.6	957.6	726.2	723.2	701.2	701.2	701.2	700.6	700.6	700.6	700.6	9.007	700.6	700.6	9.007
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Example 1; Page 31-33; 43pp; French.

Aee21942 Single ch	Aaz35704 Human gly	Ade85817 Murine in	Aat59350 1-153 del	Aat59349 1-153 c-m	Aaf30341 Bicistron	Aaf30316 Bicistron	Aeb12356 Fusion pr	Aed64236 mFc-hOGH-	Aef05391 Human mFc	Aeb12344 Immunoglo	Aed64224 Murine im	Aan91659 Chimeric	Aeb12360 Fusion pr		Aeb12362 Fusion pr	a	Aaq48037 Monoclona	Aaq54652 T84.12 He	Aav55416 Chimeric	Aav55415 Chimeric	Aat62850 Mouse sol		Ad892750 DNA encod	Aee21946 Single ch	Aaz51300 Murine im	Aaa50055 Mouse imm
AEE21942	AAZ35704	ADE85817	AAT59350	AAT59349	AAF30341	AAF30316	AEB12356	AED64236	AEF05391	AEB12344	AED64224	AAN91659	AEB12360	AED64240	AEB12362	AED64242	AAQ48037	AAQ54652	AAV55416	AAV55415	AAT62850	ADS31748	ADS92750	AEE21946	AAZ51300	AAA50055
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1509	729	1140	1158	1188	6729	7528	1530	1530	669	708	708	1341	1413	1413	1431	1431	1581	1645	1131	1194	1275	1473	1473	1524	669	669
47.2	47.2	47.2	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.0	47.0	47.0	47.0	47.0	47.0	47.0	47.0
700.4	700.2	700.2	700	700	700	700	699.4	699.4	669	669	669	669	669	669	669	669	669	669	698.4	698.4	698.4	698.4	698.4	697.8	697.4	697.4
19	20	21	22	23	24	25	36	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAF55098 standard; DNA; 1484 BP.

New soluble recombinant protein, useful e.g. as immunostimulant, comprises dimeric major histocompatibility complex molecule fused to immunoglobulin Fc region. Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin; major histocompatibility complex; Pc region; antigen; T lymphocyte; immunostimulant; vaccine; infection; tumour; ss. DNA encoding a fusion protein comprising an alpha chain of MHC. Location/Qualifiers 1. .1482 /*tag= a (CNRS) CNRS CENT NAT RECH SCI 29-JUL-1999; 99FR-00009862. 28-JUL-2000; 2000WO-FR002193. Glaichenhaus N, Malherbe L; 15-MAY-2001 (first entry) WPI; 2001-182944/18. P-PSDB; AAB67480. WO200109194-A1. 08-FEB-2001. Synthetic. AAF55098; AAPS5098
AAP

The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the FC region of an immunoglobulin. The recombinant proteins, when linked to an antigening peptide, are used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Agreactive T cells from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising an alpha chain of MHC molecules

Sequence 1484 BP; 414 A; 394 C; 362 G; 314 T; 0 U; 0 Other;

ö TGCGGAGGTGAAGACGACATTGAGGCCGACGTAGGCTTCTATGGTACAACTGTTTAT 120 CAGTCTCCTGGAGACATTGGCCAGTACACATGAATTTGATGGTGATGAGTTGTTCTAT 180 61 TGCGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTAT CAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGATGTTCTAT GTGGACTTGGATAAGAAGAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTC GAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACCAGCTGTCTTATCTCACCCTTC GGTGGAAGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAG 1 ATGCCGTGCAGCAGCACTCTGATTCTGGGGGTCCTCGCCCTGAACACCATGCTCAGCCTC GTGGACTTGGATAAGAAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTC ACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC Actaagadgreaaatrreacceageraccaargadgerecreaaggarerererere AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTC GAGACCAGCTTCCTCGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTC ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGGAGCCG GITCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACTGGA GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACTGGA Gaps ö ery Match 99.9%; Score 1484; DB 5; Length 1484; st Local Similarity 100.0%; Pred. No. 0; tches 1484; Conservative 0; Mismatches 0; Indels 0.

& g	781 GCATCTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCTCCATGCCAATGCCCAGCACCT 840
ò	841 AACCTCTIGGGIGGACCATCCGTTCATCTTCCCTCCAAAGATCAAGGAIGTACTCATG 900
QQ	841 AACCICTIGGGIGGACCAICCGICTICAICTICCCTCCAAGAICAAGGAIGTACICAIG 900
Š	01 ATCTCCCTGAGCCCCATAGTCACATGTGGTGGATGGATGTGAGCGAGGATGATGACCCAGAT 96
අු	960
& A	961 GTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGGCTCAGACACAAACCCAT 1020
&	1021 AGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGGCCCTCCCCATCCAGGACCAGGAC 1080
Ωp	1021 AGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCTCCCCATCCAGCACCAGGAC 1080
è i	1081 TGGATGGCGAGGGGTTCAAATGCAAGGTCAACAACAAGAGCTCCCAGCGCCCATC 1140
8 8	GAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCAAGGTATATGTCTTGCCT 120
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đ	1201 CCACCAGAAGAAGATGACTAAGAAACAGGTCACTGTGACCTGCATGGTCACAGACTTC 1260
& a	1261 ATGCCTGAAGACATTTACGTGGAGTGGACCAACACGGGAAAACAGAGCTAAACTACAAG 1320 1261 ATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAG 1320
ò	1321 AACACTGAACCGGTCCTGGACTCTGATGGTTCTTCATGTACAGGAAGCTGAGAGTG 1380
qa	1321 AACACTGAACCTGGACTCTGGACTCTTACTTCTTACTTCATGTACAGCTGAGGTG 1380
à	1381 GAAAAGAAGAACTGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTG 1440
qq	1381 GAAAAGAAGTGGGTGGAAAGAAATAGCTACTCTGTTCAGTGGTCCACGAGGGTCTG 1440
ò	1441 CACAATCACCACACACAAAAAGCTTCTCCCGGACTCCGGGTAA 1484
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RESU ABI9	2 1
e X :	19904
¥ ¥	199041;
5	25-FBB-2002 (first entry)
\$ E \$	Murine pCB223 coding sequence.
KW BI	Mouse; MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidabetic; antidiflammatory; antidianaemic; antitrheumatorid; antiarthritic; neuroprotective; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis; myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis; rheumatoid arthritis; systemic lupus erythematosus; ss.
\$88	Mus sp. Synthetic.
X & X	WO200170245-A1.
68	27-SEP-2001.

us-10-048-116b-3.rng

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22-MAR-2001; 2001WO-US009616.
22-MAR-2000; 2000US-0191274P.
15-MAY-2000; 2000US-0204249P.
23-JAN-2001; 2001US-0264003P.
(CORI-) CORIXA CORP.

Carter D, Zhu S, Arimilli S, Wang A;
WPI; 2001-616371/71.
P-PSDB; ABB56471.
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Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alphal and betal domain linked through amino acid linker and multimerization domain.

Disclosure, Page 115; 147pp; English.

The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alphal domain and a betal domain linked through an amino acid linker and a multimerisation domain. The first and the second molecule are linked through the multimerisation domain to form a multimeric complex, The complex is useful for treating autoimmune diaeases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomylitis (RAB), rheumatoid arthritis and systemic lupus molecule of the invention

Sequence 1676 BP; 438 A; 470 C; 407 G; 361 T; 0 U; 0 Other;

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126
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                                        96; Indels 164; Gaps
Thery Match 71.9%; Score 1067.4; DB 4; Length 1676; east Local Similarity 83.5%; Pred. No. 2.9e-277; Atches 1319; Conservative 0; Mismatches 96; Indels 164;
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qq	751	GGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGGAACTCTGGATCC	810
ò	671	CCACTACAGCTCCATC	989
Q	811	CTGTCCAGTGGTGTGCACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACCCTCAGC	870
ò	687	AGCTCAGCTCGAAAAAGGCTCCAGGCCCTGGAGAAQQAAAATGCACAGCTGGAATGGGA	746
qq	871	AGCTCAGreactGTAACCTCGAGCACCTGGCCCAGTCCATCACCTGCAATGTGG	928
ò	747	GTTGCAAGCACTGGAAAAGGAACTGGCTCAGGCATCTGAGCCCAGAGGCCCACAAT	908
Ор	929	cccacccdgcaagcagcaccaaggagcagaaaa-aarrigagcccagagggcccacaar	986
ò	807	CAAGCCTGTCCTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTT	998
Ор	987	CAAGCCCTGTCCTCCATGCAAATGCCCAGCACCTAAACCTCTTGGGTGGACCATCCGTCTT	1046
ò	867	CATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATG	926
Db	1047	CATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATG	1106
à	927	TGTGGTGGTGGATGTGAGCGAGGATGACCCAGATCCAGATCAGCTGGTTTGTGAACAA	986
QQ	1107	TGTGGTGGTGGATGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAA	1166
ò	987	CGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCG	1046
qq	1167	CGTGGAAGTACACACAGGTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCG	1226
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ò	1107	CAAGGTCAACAAAGACCTCCCAGGGCCCATCGAGAGAACCATCTCAAAACCCAAAGG	1166
qq	1287	CAAGGTCAACAACAAGACCTCCCAGCGCCCATCGAGAACCATCTCAAAACCCAAAGG	1346
ò	1167	GTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACAGAAGAAGAAGATGACTAAGAA	1226
Db	1347	GTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACAGAAGAAGAGATGACTAAGAA	1406
ò	1227	ACAGGICACTICIGACCTGCATGGICACAGACTTCATGCCTGAAGACATTTACGTGGAGTG	1286
Dp	1407	acadercacreroaccrecardercacadacrreardecreaadacarrracergaderg	1466
ò	1287	GACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGA	1346
QQ	1467	GACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGA	1526
ò	1347	TGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAAG	1406
qq	1527	TGGTTCTTACTTCATGTACAGCTGAGAGAGAAAAAAAAAA	1586
ò	1407	TAGCTACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTT	1466
qq	1587	TAGCTACTCCTGTTCAGTGGTCTGCACAATCACCACACACGACTAAGAGCTT	1646
ò	1467	CTCCCGGACTCCGGGTAAA 1485	
qq	1647	166	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This nucleotide sequences codes for a bivalent DR2 fusion protein obtained by fusion of the Pc portion of 1962a to the 3' end of a DR-alpha PCS cDNA construct (see AAV16866). The Pc portion was amplified by RT-PCR from mouse hybridoma 1243. The PCR product was then fused in frame with the DR alpha-POS construct by overlapping PCR. The DR2-19G fusion was expressed in the Drosophila Schneider cell system. The invention relates to new soluble monovalent and multivalent Class II MHC fusion proteins comprising a MHC class II binding domain and a dimerisation domain or an immunoglobulin region that can be used for the treatment of allergic and autoimmune diseases (e.g. multiple sclerosis), for tolerising a subject to foreign tissue before or after organ or tissue transplantation, or for vaccination against pathogens. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 TITATCAGICICCIGGAGACATIGGCCAGIACACACACAATITGAIGGIGAIGAGTIGI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 TCTATGTGGACTTGGATAAGAAGAAACTGTCTGGAGGCTTCCTGAGTTTGGCCCAATTGA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 TCCATGTGGATATGGCAAAGAAGGAGGGCGTTTGGCGGCGCTTGAAGAATTTGGAGTTTG 169
                                                                                                                                                                                                  mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGCTTTGAGGCTCAAGGTGCATTGGCCAACATAGCTGTGGACAAAAGCCAAACTTGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Class II MHC fusion proteins - comprising a MHC Class II binding domain and a dimerisation domain or an immunoglobulin region used for modulating immune responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 rerarergaarecraareaggggggriffargriffargaregggarrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 TACTCTTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                               Major histocompatibility complex class II; MHC class II; human; fusion procein; HIA-DR2; DRA*0101; binding domain; Fos; dimerisation domain, IGG; allergy; autoimmune disease; vaccine; multiple sclerosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ery Match 64.5%; Score 957.6; DB 2; Length 1446; Bt Local Similarity 81.8%; Pred. No. 1.2e-247; tches 1136; Conservative 0; Mismatches 234; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1446 BP; 414 A; 375 C; 356 G; 301 T; 0 U; 0 Other;
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                                                BP
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                                              AAT99707 standard; cDNA; 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0024077P
                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-US014503
                                                                                                                 (revised)
(first entry)
                                                                                                                                                                 DR2-IgG fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-159459/14.
                                                                                                                                                                                                                                                                                 Homo sapiens.
Mus musculus.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-1997;
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                                                                                                               17-OCT-2003
17-AUG-1998
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                                                                                AAT99707;
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1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAAGGGTCAGTAAGAG 1177
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                    230 TCATGACAAAGCGCTCCAACTATACTCCGATCACCAATGTACCTCCAGAGGTAACTGTGC
                                                                                                                                                                                                                                                                    TCCCCAAGTCCCCTGTGCTGGTCAGCCCAACACCCTTATCTGCTTTTGTGACAACA
                                                                                                                                                                                                                                          CAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCCATAGTCACATGTGTGGTGGTGGTGG
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                                                                                    rcaceaacaecereresaacreaeaececaacerererererereraraeacaaer
                                                                                                                    AGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAA
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TCTTGACTAAGAGGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGT
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1369
                                                          Major histocompatability complex Class II; MHC; binding domain; HIA-DR2; leucine zipper; Fos; IgG; Fc; immunoglobulin; antibody; fusion protein; multiple sclerosis; rheumatoid arthritis; graft rejection; allergy; autoimmune disease; pemphigus vulgaris; systemic lupus erythematosus; T iymphocyte; T cell; diagnosis; therapy; adoptive immunotherapy; ss.
1310 TCATGTACAGCAAGCTGAGAGTGGAAAAGAACTGGGTGGAAAGAATAGCTACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New HMC Class II binding domain fusion proteins and conjugates - used for, e.g. treating allergic and autoimmune diseases or detecting, isolating, activating or killing specific T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "alpha-mating factor secretion signal"
16. 1437
/product= "DR2-Fos-Fo"
                                                                                                                                                                                                                                                                                                                                                                                                                              HLA-DR2 alpha-Fos-IgG fusion construct.
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1. .1440
/*tag= a
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/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                               CGGGTAAA 1485
                                                                                                                                                                                       1430 CGGCTAAA 1437
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Saccharomyces c
Synthetic.
Chimeric.
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                                                                                                                                               1478
                                                                                                                                                                                                                                                                                                                                         AAX87813;
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CDS
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This nucleotide sequence codes for a divalent HIA-DR2 MHC binding domain fusion protein (see AAY31654) comprising an alpha-mating factor secretion signal, the extracellular domain of the HIA-DR2 alpha chain (residues 1-191 of DRA*0101), a 7-amino acid linker, the 40-amino acid leucine zipper dimerization domain of Fos, and the Fc portion of 1gG2a. The DR-alpha-Fc chain corresponds to an antibody heavy chain. The invention provides new monovalent, multivalent and multimeric MHC Class II binding domain fusion proteins and conjugates comprising at least a binding domain of an MHC

Example 7, Page 100-102; 113pp; English.

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Class II alpha or beta chain and a dimerization domain, especially a Fosor or Jun leucine zipper domain. The MHC fusion proteins and conjugates can be used if for detecting and isolating T cells having a defined MHC/peptide complex specificity (claimed); to confer to a subject adoptive immunity to a defined MHC/peptide complex (claimed) is to stimulate or activate T cells reactive to a defined MHC/peptide complex (claimed); for selective killing of T cells reactive to a defined MHC/peptide complex (claimed); to treat claiming of T cells reactive to a defined MHC/peptide complex (claimed); to treat allergic and autoimmune diseases, e.g. multiple sclerosis, rheumatoid arthitis, pemphigus vulgaris, and systemic lupus erythematosus; and to prevent organ or tissue transplant rejection. The DR2-IgG design was chosen to increase the affinity for the T cell receptor by increasing valency, and to attach an effector domain, the Rc region of IgG2a.

Complement fixation may result in the lysis of target T cells following binding of DR2-IgG molecules can any therefore be useful for the selective depletion of autoaggressive T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 ICATGIGGATATGGCAAAGAAGAAGGACGGTCTGGCGGCTTGAAGAATTTGGACGATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.5%; Score 957.6; DB 2; Length 1446; Best Local Similarity 81.8%; Pred. No. 1.2e-247; Matches 1136; Conservative 0; Mismatches 234; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1446 BP; 414 A; 375 C; 356 G; 301 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel class II major histocompatibility complex (MHC) fusion protein having MHC class II binding domain of MHC class II alpha chain, and dimerization domain, useful for treating pemphigus vulgaris, rheumatoid
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Pred. No. 4.1e-185;
0; Mismatches 323; Indels 135;
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23-JAN-2001; 2001US-0264003P.
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                                CTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGAGTTGTTCTATGTGGACT
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The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alphal domain and a betal domain linked through an amino acid linker and a multimerisation domain. The first and the second molecule are linked through the multimerisation domain to form a multimeric complex, The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (RAB), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention

Sequence 2343 BP; 562 A; 665 C; 635 G; 481 T; 0 U; 0 Other;

953 CCCAAGGTGGACTGCAAAACATAGCTACAGGAAAATACACCTTGGGAATCTTGACTAAGA 1012 1073 crerecrecrescreasceceaececrearerecrerrereseaeaeaererrecreere 1132 1133 TGATCAACATCACATGGCTCAGAAATAGTAAGTCAGTCACAGACGGCGTTTATGAGACCA 1192 1193 GCTTCCTTGTCAACCGTGACCATTCCTTCCACAAGCTGTCTTATCTCACCTTCATCCCTT 1252 1433 GATGCCTGGTCAAGGCCTATTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCC 1492 1013 GGTCAAATTCCACCCAGCTACCAATGAGGCTCCTCAAGGGACTGTGTTCCCCAAGTCCC 1072 1313 AACACTGGGGCTAGCGGAGGGGGGGGAAGCGGAGGAAGCTTAGCCAAAACGACACCCC 1372 1493 TGTCCAGCGGTGTGCACACCCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGAGCA 1552 68 GTGAAGACGACATTGAGGCCGACCACGTAGGCTTCTATGGTACAACTGTTTATCAGTCTC 127 128 CTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGATGATTGTTCTATGTGGACT 187 CCCAAGGTGGACTGCAAAACATAGCTGCAGAAAACACAACTTGGGGAATCTTGACTAAGA 307 367 427 607 792 832 892 487 547 655 ----ACTGGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCA 710 732 188 TGGATAAGAAAAACTGTCTGGAGGCTTCCTGAGTTTGGCCAATTGATACTCTTTGAGC 247 GGTCAAATTTCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCCAAGTCCC CTGTGCTGCTGGGTCAGCCCAACACCCTTATCTGCTTTGTGGACAACATCTTCCCACCTG 548 CTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTTGAGGAGCCGGTTCTGA 733 CAGCTGGAATGGGAGTTGCAAGCACTGGAAAGGAACTGGCTCAGGCAGCATCTGAGGCCC TGATCAACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTATGAGACCA Indels 138; Gaps Length 2343; 0; Mismatches 323; DB 4; 617 -AACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAA 48.7%; Score 723.2; DB 4, 70.4%; Pred. No. 2.6e-184 711 GGCCCTGGAGAAGGAAAT----608 AACACTGGG----uery Match Best Local Similarity 70.4 Watches 1095; Conservative 248 368 308 428 488

CCAGCGAGACCGTCACCTGCAACGTTGCCC 161	GCAAATGCCCAG 835	 AATTGTGCCCAGGGATTGTGGTTGTAAGC 1673	CGTCTTCATCTTCCTCCAAAGATCAAGG 889	reterreterececeaageceaage 1733		10		TCTCCGGGTGGTCAGTGCCCTCCCCATCC 1069	 TTTCCGCTCAGTCAGTGAACTTCCCATCA 1913		-	 CAAAGGCAGACCGAAGGCTCCACAGGTGT 2032	TAAGAAACAGGTCACTCTGACCTGCATGG 1249	CAAGGATAAAGTCAGTCTGACTGA 2092	GGAGTGGACCAACGGGAAAACAGAGC 1309	deadrescagresaarescasceasces 2152		177	DAGAAATAGCTACTCCTGTTCAGTGGTCC 1429 	GAGCTTCTCCCGGACTCCGGGTAAA 1485	IIII IIIIII GAGCCTCTCCCACTCTCCTGGTAAA 2328				quence.	thritic; antidiabetic; ogical; antinflammatory; in G; ds; gene.		.2a"
) GCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCA		ACCCGGCCAGCACCAAGGTGGACAAGAAATTGTGCCCAGGGATTGTGGTTGTAAGC	5CACCTAACCTCTTGGGTGGACCATCGTCCTTCATCTTCCCTCCAAAGATCAAGG		ATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGTG			CACAAACCCATAGAGAGATTACAACAGTACTCTCGGGGTGGTCAGTGCCCTCCCCATCC		AGCACCAGGACTGGATGGCAAGGAGTTCAAATGCAAGGTCAACAACAACAAGACCTCC			ATGTCTTGCCTCCACAGAAGAAGATGACTAAGAAACAGGTCACTCTGACCTGCATGG		TCACAGACITCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAAACAGACG		TABACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCA		D AGCTGAGAGTGGAAAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCC		ATGAGGGCTGCACACCACATACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA	standard; DNA; 1045 BP.		:004 (first entry)	protein WT-IL-15-mlgG2a coding se	immunosuppressive, antirheumatic, antiarthritic neuroprotective, antipsoriatic, dermatological, cytostatic, interleukin-15, immunoglobulin G, d	c. fied.	Location/Qualifiers 11044 /*teg= a /product= "WT-IL-15-mlgG" /transl except
1553	793	1613	836	1673	890	Ĺ	6	1010	1853	1070	1130	1973	1190	2033	1250	2093	31	Ţ	1370	1430	2273	LT 8 7566 ADO07566	AD007566	15-JUL-2	Fusion p	immunosu neuropro cytostat	Syntheti Unidenti	Key CDS
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The present invention relates to a fusion protein consisting of wild-type interleukin-15 (IL-15) and an immunoglobulin G (IgG) Fc fragment, other than a murine IgG2b Fc fragment. The fusion proteins and coding sequences are used to prevent or treat consequences of transplantation and/or autoimmune diseases, e.g. rheumatoid arthritis, diabetes, multiple sclerosis, psoriasis, neurodermatitis, ulcerative colitis, tumours and AIDS, etc., and tissues or organs that express the protein are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion protein of interleukin-15 and Pc fragment, useful for treating e.g. transplantation disorders, autoimmune diseases and tumors, also related nucleic acid.
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                      1180 CCACAGGIATATGICTIGCCTCCACCAGAAGAGAGAGATGACTAAGAAACAGGICACTCTG
                                                                                                        736 CCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAAGATGACTAAGAAACAGGTCACTCTG
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                                                                                                                                                                                                                                                                                                                      immunosuppressive; antirheumatic; antiarthritic; antidiabetic; neuroprotective; antipsoriatic; dermatological; antiinflammatory; cytostatic; interleukin-15; immunoglobulin G; ds; gene; human.
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Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a fusion protein consisting of wild-type interleukin-15 (IL-15) and an immunoglobulin G (IgG) Fc fragment, other than a murine IgG2b Fc fragment. The fusion proteins and coding sequences are used to prevent or treat consequences of transplantation and/or autoimmune diseases, e.g. rheumatoid arthritis, diabetes, multiple sclerosis, psoriasis, neurodermatitis, ulcerative colitis, tumours and AIDS, etc., and tissues or organs that express the protein are useful for transplants. Also transpend animals, as allo, auto. or xenotransplants. Also transgenic animals that express the fusion proteins are useful as source of cells, tissues and organs for transplantation or to screen for pharmaceuticals and/or to identify toxic substances. The present sequence is a polypeptide coding sequence used in the
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P-PSDB; ADO07559.
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immunosuppressive, antirheumatic, antiarthritic, antidiabetic, neuroprotective, antipsoriatic, dermatological, antiinflammatory; cytostatic, interleukin-15, immunoglobulin G, ds, gene.

Pusion protein coding sequence fragment Igk8

(first entry)

15-JUL-2004

AD007577;

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transplantation into humans or other mammals, as allo., auto- or xeno-
transplants. Also transgenic animals that express the fusion proteins are
useful as source of cells, tissues and organs for transplantation or to
screen for pharmaceuticals and/or to identify toxic substances. The
present sequence is a coding sequence used in the exemplification of the
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                                                                                                                                                        Sequence 1108 BP; 343 A; 255 C; 253 G; 257 T; 0 U; 0 Other;
                                                                                                                 invention.
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Dreher I,

WPI; 2004-357203/33.

14-OCT-2002; 2002EP-00022869.

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Synthetic. Unidentified

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BP

AD007577 standard; DNA; 1108

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The present invention relates to a fusion protein consisting of wild-type interleukin-15 (IL-15) and an immunoglobulin G (IgG) Pc fragment, other than a murine IgG2b Pc fragment. The fusion proteins and coding sequences are used to prevent or treat consequences of transplantation and/or autoimmune diseases, e.g. rheumatoid arthritis, diabetes, multiple sclerosis, psoriasis, neurodermatitis, ulcerative colitis, tumours and AIDS, etc., and tissues or organs that express the protein are useful for transplantation into humans or other mammals, as allo, auto- or xeno-transplants. Also transgenic animals that express the fusion proteins are useful as source of cells, tissues and organs for transplantation or to screen for pharmaceuticals and/or to identify toxic substances. The present sequence is a coding sequence used in the exemplification of the
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New fusion protein of interleukin-15 and Pc fragment, useful for tree e.g. transplantation disorders, autoimmune diseases and tumors, also related nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1108;
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Pred. No. 1.7e-178;
0; Mismatches 53; Indels
                                                                                                                                       Disclosure, Fig 10, 63pp; German.
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Best Local Similarity 93.3%;
Matches 733; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             919 AAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTC
                                                                                      619 CTCCCCATCCAGCACCAGGACTGAGTGAGTGAGAGTCAAATGCAAGGACAACAC
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                                                                                                                                                                        739 AAAGACCTCCCAGCGCCCATCGAGAGCCATCTCAAAACCCAAAGGGTCAGTAAGAGCT
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18-SEP-2002; 2002US-0411974P.
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New polypeptide comprises a sequence of amino acids that is selectively reactive with beta-amyloid peptide 42 or at least one complementarity-

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This invention relates to novel methods and compositions for detecting and modulating beta-amyloid (A-beta) peptide levels and the processing of amyloid beta A precursor protein (APP). Specifically, it refers to methods of assessing the presentlin activity of compounds using the lipoprotein receptor related protein (LRP), in order to identify to presentlin proteins that can be used to affect the processing of APP. The presentlin proteins that can be used to affect the processing of APP. The presentlin activity and A-beta levels, in particular beta-amyloid 42 (A-beta 42), such that the agent is selectivity reactive with A-beta 42 and binds at least one complementarity determining region (CDR) of either antibody A387 or antibody 8436. As such, the polypeptides, nucleic acids and antibodies are useful for treating Alzheimer's disease, accordingly the compositions exhibit neuroprotective and nootropic activities. This polymucleotide sequence is a murine antibody chain DNA fragment of the invention.
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treating
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                                                                                                                                                                                                                                                                                                                       47.2%; Score 700.6; DB 12; Length 990; 100.0%; Pred. No. 2.3e-178; artive 0; Mismatches 0; Indels 0;
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 for
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 useful
antibody A387 or B436,
                                          Disclosure; SEQ ID NO 68; 408pp; English
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Matches 700; Conservative
 region of disease.
  determining
Alzheimer's
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us-10-048-116b-3.rng

951 TCACCACACGACTAAGAGCTTCTCCCGGACTCCGGGTAAA 990

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antitheumatic; antithroid; bon metatases; calcium antagonist; cancer; cardiovascular-gen.; degeneration; eating-disorders-gen.; endocrine den.; endocrine-gen.; endocrine-gen.; gastrointestinal-gen.; gene; genetic disorder; heavy chain; hepatotropic; hypercalcenta; immune disorder; heavy chain; hepatotropic; hypercalcenta; endouth disease; musculoskeletal disease; moplaem, nephrotropic; osteopetrosis; osteopetrosis; pagets disease; periodontal disease; pharmaceutical; rheumatold arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                  endocrine-gen.; antiarthritic; antibacterial; antiinflammatory;
                                                                                                                                                                                                                                                                                            M-CSF specific murine antibody RX1 heavy chain cDNA.
AEC20762 standard; cDNA; 1401
                                                                                                                                                                                            20-OCT-2005 (first entry)
                                                                                           AEC20762;
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Mus musculus

WO2005068503-A2.

28-JUL-2005

06-JAN-2005; 2005WO-US000546.

07-JAN-2004; 2004US-0535181P. 02-JUN-2004; 2004US-0576417P.

(CHIR) CHIRON CORP. (XOMA) XOMA TECHNOLOGY LTD.

Liu C, Zimmerman DL, Harrowe GM, Koths K, Kavanaugh WM, Long L; Calderon-Cacia M, Horwitz AH;

2005-597707/61. P-PSDB; AEC20763

for Novel non-murine antibody that competes with monoclonal antibody RXI binding to macrophage colony stimulating factor, useful for treating hypogonadism, hypercalcemia, rickets, scurvy, homocystinuria, cancer, osteoporosis.

Claim 67; SEQ ID NO 1; 269pp; English.

The invention describes a non-murine antibody (I) that competes with monoclonal antibody RX1 for binding to macrophage colony stimulating factor (M-CSF) by more than 75t, where the monoclonal antibody RX1 has the heavy chain and light chain amino acid sequences having a fully defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4) sequences given in the specification, respectively. (I) is useful for preventing a subject afficted with a disease that causes or contributes to osteolysis, where the antibody effectively reduces the severity of bone loss associated with the disease. The disease is chosen from metabolic bone diseases associated with relatively increased osteoclast activity, including endocrinopathies, hypercalcemia, deficiency states, chronic diseases, and hereditary diseases, cancer, osteoporosis, osteoperosis, inflammation of bone associated with arthritis and rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or paget's disease. (I) is useful for preventing or treating metastatic cancer. Antibodies of the invention are useful for preventing or reducing bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is useful for sease that causes or contributes to osteolysis, and metastatic cancer the bone in a patient for meanifecturing a medicament for preparing a patient while cancer, for manufacturing a medicament for treating apatient having cancer. (I) in synergistic combination, is useful for preparing a

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medicament for treating a patient exhibiting osteolysis. This sequence encodes macrophage colony stimulating factor (M-CSF) specific murine antibody RX1 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                 822 CCTGAGCCCCATAGTCACATGTGTGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA
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                                                                                                                                                     Gapa
                                                                                                               Length 1401;
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                                                                            Sequence 1401 BP; 369 A; 407 C; 327 G; 298 T; 0 U; 0 Other;
                                                                                                           Query Match
47.2%; Score 700.6; DB 14; Length
Best Local Similarity 100.0%; Pred. No. 2.7e-178;
Matches 700; Conservative 0; Mismatches 0; Indels
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1330 TGAAGACATTTACGTGGAGTGGACCAACAGGGAAAACAGGGAAAACTGAAGAAGAACT 1389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; gene; immunostimulant; immunogenicity; antibody.
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P-PSDB; ADV26107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes an agent (I) for treating prion disease or delivering a subtance to the lesioned region of prion disease, comprising a mesenchymal cell. Also described are: a nucleic acid (II) having an anti-prion antibody gene comprising: an antibody heavy chain gene having SEO ID No: 1, 3, 5, 30, 32 and 34, an unclectide sequence consisting of a degenerate genetic code, which encodes a polypeptide same as that of the above sequences, or anuclectide sequence, which is a mutant of the above sequences, and an antibody light chain gene having SEO ID No: 2, 4, 6, 31, 33 and 35, a nuclectide sequence first is conditions with the above sequences; and an antibody light chain gene having SEO ID No: 2, 4, 6, 31, 33 and 35, a nuclectide sequence having SEO ID No: 2, 4, 6, 31, 33 and 35, a nuclectide sequence formations with the above sequences, and anclectide sequence for an antibody light chain gene conditions with the above sequences, or a nuclectide sequence which is a mutant of the above sequences, or a nuclectide sequence that is complementary to the above sequences and that hybridizes under stringent conditions with the above sequences, a nuclectide sequence that is anti-prion chimeric antibody (IV) comprising variable region of antibody encoded by (II) and constant region of antibody of animal other than mouse; a nuclet acid that encodes (IV); preparing (II) or clink and activity to the cell, a cell (IV) having abnormal prion proliferation inhibition activity, occurring of a prion disease, and obtainable by (MI) or by utilizing (II) or (III); a senting prion disease, and editoring a substance to the lesioned region of prion disease, and delivering a substance to the lesioned region of prion disease, and delivering a substance to the lesioned region of prion disease, and delivering a substance to the lesioned region of prion disease, and delivering a substance to the lesioned region of prion disease, and delivering a substance to the lesione coll is maching abnormal prion pridieration inhibition service an
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                                                                                                                                                                                                                                                                                                                                                                                 Agent useful for treating prion disease or delivering a substance to a lesioned region of prion disease, comprises a mesenchymal cell.
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47.2%; Score 700.6; DB 14; Length 1560;
st Local Similarity 100.0%; Pred. No. 2.8e-178;
tcheg 700; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                  Hamada H, Horiuchi
                                                                                                                                                                                                                                                             Fujinaga K, Shinagawa M, Niitsu Y,
Honmou O, Umetani A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; SEQ ID NO 5; 34pp; Japanese.
                                                                                                                        30-MAR-2005; 2005WO-JP006189.
                                                                                                                                                                      30-MAR-2004; 2004JP-00100649
                                                                                                                                                                                                                    (RENO-) RENOMEDIX INST INC
                                                                                                                                                                                                                                                                                                                                     WPI; 2005-725409/74.
                                 WO2005094846-A1.
                                                                               13-OCT-2005.
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28-MAY-2004; 2004WO-US017005 30-MAY-2003; 2003US-0475202P.

WO2005007809-A2 27-JAN-2005.

Mus sp. Synthetic.

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The invention relates to a de-immunized anti-CD3.antibody. The antibod composition and methods are useful for stimulating an immune response against infections and for treating infections. The present sequence represents DNA encoding mouse OKT3 VH.
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                                                                                                                                                                                                    uery Match 47.2%; Score 700.6; DB 14; Length 1569; isst Local Similarity 100.0%; Pred. No. 2.8e-178; atches 700; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                               Sequence 1569 BP; 446 A; 443 C; 356 G; 324 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1446 TCACCACACACTAAGAGCTTCTCCCGGACTCCGGGTAAA 1485
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fusion protein; IgG; antibody; antiinflammatory; antimicrobial-gen.; cytokine release syndrome; inflammation; infection; ds; gene.
                                                                                                                                                   heavy chain variable region DNA.
ם
ADW71834 standard; DNA; 1569
                                                                                                    (first entry)
                                                                                                    07-APR-2005
                                                                                                                                                      Murine OKT3
                                                    ADW71834;
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The invention relates to a novel fusion protein, comprising a non-FC component and an FC region having a first portion derived from one or more human 1gG4 antibodies and a second portion derived from one or more human 1gG4 antibodies. The invention further comprises: a method for reducing antibody-mediated cell activation or inflammation events, comprising antibody-mediated cell activation or inflammation events, comprising antibody-mediated cell activation or inflammation events, comprising antibody including an engineered heavy chain constant region having a first portion derived from one or more human 1gG2 antibodies and a second coption derived from one or more human 1gG2 antibodies and a second coption derived from one or more human 1gG2 antibodies and a second correasing the half life of a non-FC component, increasing the avidity of increasing the half life of a non-FC component, increasing the avidity of component for a molecule to which the non-FC component binds, correction, or improving expression of a non-FC component in mammalian cells creceptor binding and complement activation associated with a FC fusion protein, or improving expression of a non-FC component in mammalian cells containing the nucleic acid, a host cell transfected with an expression containing the nucleic acid, a host cell transfected with an expression containing the nucleic acid, a host cell transfected with an expression creceptor, and a composition comprising the fusion protein are useful in preventing or reducing antibody-mediated cell activation or release syndrome, and in reducing antibody-mediated cell activation or release syndrome, and in reducing antibody-mediated cell activation or composition, methods are useful for preventing or the invention. This composition, methods are useful for preventing infections. This composition, methods are useful for preventing of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATCAGCTGGTTTGTGAACAACGTGGAAGTACACAGGCTCAGACACACAAACCCATAGAGA 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    864 ccreadececearagecaracides de residentes de des des de cercadas de compandades de compandades
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reducing antibody-mediated cell activation or inflammation events, useful for preventing infections, comprises administering an antibody including an engineered constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTIGGGIGGACCAICCGICTICAICTICCCTCCAAAGAICAAGGAIGIACTCAIGAICTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Squinto SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, SEQ ID NO 18; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rother RP, Faas-Knight S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 100. Matches 700; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-112860/12.
P-PSDB; ADW71833.
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May 31, 2006, 23:41:05; Search time 657.424 Seconds (without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaf55099 DNA encod	Aat04262 Hybrid IA	Adq31225 I-Ab(beta	Aat04269 Hybrid IA	Adq31228 I-Ab(beta	Aat86989 SCE1 sing	Aca60744 Mouse MHC	Aat86987 SSC1 sing	Aca60742 Mouse MHC	Aat86988 SCT1 sing	Aax89069 Single ch	Aca60743 Mouse MHC	Aat17588 Vector SC	Aat17586 Vector SS	Aat17587 Vector SC	Aav12068 Murine IA	Adj75986 Marker ge	Adx26090 Novel cel
	1																		
SUMMARIES	Δĭ	AAF55099	AAT04262	ADQ31225	AAT04269	ADQ31228	AAT86989	ACA60744	AAT86987	ACA60742	AAT86988	AAX89069	ACA60743	AAT17588	AAT17586	AAT17587	AAV12068	ADJ75986	ADX26090
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	Length	921	893	945	1013	915	1382	1382	1385	1385	1508	1508	1508	1382	1385	1508	4724	798	798
	Query Match	96.8	74.6	69.9	68.1	66.1	63.9	63.9	63.9	63.9	63.9	63.9	63.9	63.7	63.7	63.7	62.9	59.1	59.1
	Score	921	709.2	665.2	648	628.6	607.8	607.8	607.8	607.8	607.8	607.8	607.8	606.2	606.2	606.2	598.6	561.8	561.8
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Example 1; Page 34-35; 43pp; French.

Abi99040 Murine pC	Aag03170 Seguence	Aat06286 I-Ab-beta	Aaq56920 Mouse I-A		Abi99038 Murine pC			MBP	Abi99028 IAS MBP 1	Abi99032 MBP 1-14	Ab199027 IAS MBP 1	Abi99021 I-AB MBP.	Ab199030 IAS MBP 9	Abi99029 IAS MBP 9	Abi99033 MBP 90-10	Abk63510 Rat seque	Adb57995 Toxicity-	Abt41775 Toxicity		Adv40851 Rat cardi	Adx25826 Novel cel	Adq38634 Human SNP	Adq38637 Human SNP	Abk84087 Human cDN	Abx63009 Human cDN	Aad63150 Human maj
ABI99040	AAQ03170	AAT06286	AAQ56920	AAQ35055	ABI 99038	ABN84048	AB199039	AB199031	ABI99028	AB199032	ABI99027	AB199021	ABI99030	AB199029	AB199033	ABK63510) ADB57995) ABT41775	L ADW21868	3 ADV40851	1 ADX25826	3 ADQ38634	1 ADQ38637	ABK84087	ABX63009	AAD63150
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1085	702	702	702	702	1698	1243	1662	1686	1701	2059	2346	1680	1707	2053	2343	562	295	562	562	562	562	1869	1892	1171	1199	1192
57.8	57.0	57.0	57.0	56.3	55.2	52.8	52.5	52.3	52.3	52.3	52.3	52.2	52.2	52.2	52.2	45.6	45.6	45.6	45.6	45.6	45.6	43.6	43.6	43.2	43.2	42.9
549.8	542	542	542	535.6	525.4	502.6	499.4	497.2	497.2	497.2	497.2	496	496	496	496	433.6	433.6	433.6	433.6	433.6	433.6	414.8	414.8	410.8	410.8	407.6
19	50	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAF55099 standard; DNA; 921 BP

RESULT 1

AAF55099;

New soluble recombinant protein, useful e.g. as immunostimulant, comprises dimeric major histocompatibility complex molecule fused to immunoglobulin Fc region. Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin; major histocompatibility complex; Fc region; antigen; T lymphocyte; immunostimulant; vaccine; infection; tumour; ss. DNA encoding a fusion protein comprising a beta chain of MHC. Location/Qualifiers (CNRS) CNRS CENT NAT RECH SCI 29-JUL-1999; 99FR-00009862. 28-JUL-2000; 2000WO-FR002193 Glaichenhaus N, Malherbe L; 15-MAY-2001 (first entry) 1. .921 /*tag= WPI; 2001-182944/18. P-PSDB; AAB67481. WO200109194-A1 08-FEB-2001. Synthetic. Key

The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the Fc region of an immunoglobulin. The recombinant proteins, when linked to an antigenic peptide, are used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Ag-reactive T cells from cell cultures or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising a beta chain of MHC molecules

Seguence 921 BP; 214 A; 265 C; 286 G; 156 T; 0 U; 0 Other;

ö 140 200 260 320 420 480 560 620 720 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCGGGGGCAAG 800 240 380 440 500 540 909 680 99 740 301 raccacaccaccarcerecentracecedereaceseareseeceseeceseeceseeceses 360 9 GTCATGCTGGAGATGACCCCTCATCAGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 1 ATGGCTCTGCAGATCCCCCAGCCTCCTCTCAGCTGCTGTGTGGTGCTGATGGTGCTGT AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC GETGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 361 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGAACACGGCGTGC GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACACACTCTGGTCTGTTCG GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAAAAACTCTGGTCTGTTCG GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG GTGACAGATITCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG ACAGTGGGGGTCTCATCCACACACTGTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG ACAGTGGGGTCTCATCCACACGTTATTAGGAATGGGGACTGGACCTTCCAGGTCCG 21 ATGGCTCTGCAGATCCCCCAGCCTCCTCTCAGCTGCTGTGGTGGTGATGGTGCTG ATCGTGGTGTCCCGCCAGCTGGGACGTGGGGGCTCACTAGTGCCCCCGAGGCTCTGGA GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGCGTGC AGACACAACTACGAGGGCGGGAGACCAGCACCTCCCTGCGGCGCGTTGAACAGCCCAAT GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 0; Gaps Length 921; 0, Indels ery Match 96.8%; Score 921; DB 5; Le t. Local Similarity 100.0%; Pred. No. 8.4e-205; tches 921; Conservative 0; Mismatches 0; 121 481 61 621 601 741 81 141 201 181 261 241 321 381 441 501 561 541 681 661

à	801 GGAG	GTGGAGGATCCACTACAGCTCCATTGAAAAAAAAATTGCAAGCACTG 860
셤	 781 GGAG	
ò	861 AAGA	AAGAAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTCGCCCAG 920
q	841 AAGA	AAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAACTCGCCCAG 900
È	921 CATC	CATCATCATCATCATTGA 941
요	901 CATC	ATCATCATCATTGA 921
RESULT AAT0420 ID A	T 2 262 AAT04262	standard; DNA; 893 BP.
χX	AAT04262;	
ጀቴ፧	16-APR-1996	(first entry)
X B	Hybrid IA beta	beta chain gene.
X	Polymerase chi major histocor autoimmune di immunoprolife	Polymerase chain reaction; PCR; primer; amplify; major histocompatability complex; MHC; T-cell receptor; TCR; autolmmune disease; immunodeficiency disease; immune response; immunoproliferation disease; graft-host rejection; therapy; ss.
X 8	Synthetic.	
žet	Key primer bind	Location/Qualifiers
FE	primer_bind	/*tag= a /note= "probable primer binding site (primer #233)" complement(4574)
H H H	Subs	/*tag= b /note= "binding site for primer #261 (see AAT04260)" 61. 828
FF	3	/*tag= c /product= "hybrid IA beta chain"
11	sig_peptide	61141 /*tag= d
223	primer_bind	/note= "leader region" complement (119172)
	primer_bind	/notes "binding site for primer #331 (see AAT04261)" complement (158212)
	primer_bind	/"tag= I primer #332 binding site" complement(199250)
FFF	misc feature	/*tag= g /note= "primer #333 (see AAT04263) binding site" 371389
FE	mat peptide	/*tag= h /note= "probable primer binding site (primer #270)" 511825
EEE	primer bind	/*tag= i /product= "IA beta chain beta 2 region" 521550
###	primer_bind	<pre>/*tags j /note= "probable primer binding site (primer #271)" 532554</pre>
EEE	primer_bind	/*tag= K /note= "probable primer binding site (primer #272)" /************************************
	primer_bind	primer binding site (primer #259)
£ X 3	TA-418FC290W	<pre>/note= "probable primer binding site (primer #232)"</pre>
ī	**************************************	

692

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787

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The invention relates to a novel class II major histocompatibility complex (MHC) antigenic peptide composite comprising a peptide containing the T-cell antigenic determinant of a mucous membrane invasive protein and the extracellular region of a class II MHC molecule or at least part of the extracellular region of the class II MHC molecule having an amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide-Class II major histocompatibility complex (MHC) composite, useful for detecting antigen specific CD4+ T-cell, comprises antigen peptide containing epitope of mucous membrane invasive protein, and extracellular region of MHC.
                                                                                                                                                                                                                                                                                                                                                  693 CTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCA 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I-Ab(beta)-Cholera toxin B subunit-leucine zipper (LZ)-BirA fusion cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    class II major histocompatibility complex; MHC; CD4+ T-cell detection;
flow cytometry; mucous membrane invasive antigen;
I-Ab (beta)-cholera toxin B subunit-leucine zipper-BirA fusion; CTB; ss;
gene.
                                                                                                                                                                                                                                                                                                                           TGTGGAGCATCCCAGCCTGAAGAGCCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTC
633 redecadeadeadacadrededegrerearecadadacrearradeaareggaacregad
                                                                                                           573 reregreregreacagarrecraceagecaagareaagreegeregreeregaa
                                                                                                                                                      TGGCCAGGAGGAGACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGAC
                                                                                                                                                                                                                                        CTTCCAGGTCCTGGTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "I-Ab(beta)-Cholera toxin B subunit (CTB)-
leucine zipper (LZ)-Bira fusion cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SENT-) SENTAN KAGAKU GLJUTSU INCUBATION CENT KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 10; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                TGCCCGGAGCAAGGGAGGTGGAGG 811
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADQ31225 standard; cDNA; 945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-546819/53.
P-PSDB; ADQ31224.
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Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a hybrid IA beta chain gene, containing the chicken ovalbumin peptide (cOVA). This sequence was used in the construction of a hybrid in alpha beta dimer. The encoded protein (pladeoVA) was found to be more stable than the IA alpha beta dimer. The stability was decreased by the addition of a MHC groove specific binding peptide (e.g. see ARR82527, ARR82528 and ARR82511), compared to an increase seen on the addition of a MHC binding peptide to IE k/d-MCC. These complexes may be used to regulate an immune response. The complexes are capable of being recognised by a TCR alone or in combination with additional MHC proteins. These complexes are useful for therapeutic purposes and experimental purposes. They can also be used as reagents for the treatment of diseases including autoimmune diseases, immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 GGAATTCTTAGAGATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGGT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTACTACACCAACGGGACGCACATACGGCTCGTGACCAGATACATCTACAACCGGGA 307
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                                                                                                                                                                                                                                                                                                       Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 GCTGATGGTGCTGAGCCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 GCTGATGGTGCTGAGCCCCCGGGACTGAGGCCGGAAACTCC----GTACATGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 GCTGGAGCACCCGATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGAGGCTCTGGAGGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lery Match
74.6%; Score 709.2; DB 2;
set Local Similarity 94.7%; Pred. No. 2.1e-155;
stches 761; Conservative 0; Mismatches 28;
                                                                                                                                                        (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 53; 94pp; English.
                                                                   95WO-US002689
                                                                                                             94US-00207481
                                                                                                                                                                                                Marrack P;
                                                                                                                                                                                                                                        WPI; 1995-320543/41.
P-PSDB; AAR82533.
                                                                   03-MAR-1995;
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                                                                                                                                                                                                Kappler JW,
                             08-SEP-1995
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us-10-048-116b-5.rng

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acid sequence comprising one or more deletions, substitutions or additions. The molecule of the invention may be useful for detecting an antigen-specific CD4+ T-cell by flow cytometry and for presenting a microorganism-derived mucous membrane invasive protein as an antigen. The method of the invention enables efficient detection of antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence is that of the class II major histocompatibility complex-related I-ho(alpha)-Cholera toxin B subunit (CTB)-leucine zipper (LZ)-BirA fusion cDNA of the invention.
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Seguence 945 BP; 230 A; 256 C; 294 G; 165 T; 0 U; 0 Other;

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                                                                                                                                               123 CCGTCGCTGGAGCACCCGGATCGTGGTGCTCCGGCAGCTGGGAGGTGGGGCTCACTA
                                                                                                                                                                      109 AATAAGACGCCGCACGCGATCGCGGCCATCAGCATGGCGAACGGAGGTGGTGGTGGTCGGT
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                                                                        GTGGTGATGGTGAGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCG
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                                         Gaps
                                       6
     Length 945;
/ Match 69.9%; Score 665.2; DB 12; Length Local Similarity 86.6%; Pred. No. 3.8e-145; Ae 759; Conservative 0; Mismatches 108; Indels
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/*tag= e
/note= "binding site for primer #363 (see AAT04271)"
complement(177. .226)
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/octe= "binding site for primer #362 (see AAT04270)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tags m
/notes "probable primer binding site (primer #366)"
/notes notes primer binding site (primer #59)"
/notes "probable primer binding site (primer #59)"
                                                                                                                                                                                                                                                                                                                                                                                 %45. .403
385. .403
7.403
//tea= h
//nobable primer binding site (primer #270)"
//tea= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "probable primer binding site (primer #271)"
544. .568
/*tag= k
/*tag= k
923. .850
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/note= "probable primer binding site (primer #259)"
942. .976
                                                                                                                                                                                       site'
                                                                                                                          Major histocompatability complex; MHC; T-cell receptor; TCR; autoimmune disease; immunodeficiency disease; immune response; immunoproliferation disease; graft-host rejection; therapy; B M12.C3; pM12-IAb-Ea; ss.
                                                                                                                                                                                                                                                                                                                                                                        /*tag= g
/note= "primer #365 (see AAT04272) binding
                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "IA beta chain beta 2 region"
535. .564
                                                                                                                                                                                                                                                    /*tag= c /product= "hybrid IA beta chain" /product= "hybrid IA beta chain" /*tag= d /note= "leader region" /complement(140. .191)
           915
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/note= "primer #364 binding site"
complement(212. .266)
BP.
                                                      standard; DNA; 1013
                                                                                          (first entry)
                                                                                                          Hybrid IA beta chain gene
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04-MAR-1994;

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JP2004196789-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a hybrid IA beta chain gene. This sequence contains a fragment of the IB alpha chain (residues 56-73), sa well as a linker and cleavage lite. This sequence was transfected into a B cell line (M12.C3) using plasmid pM12-IAb-EB. It was found that the encoded sequence was expressed in these cells. Complexes such as this may be used to regulate an immune response. The complexes are capable of being recognised by a TCR alone or in combination with additional MiC proteins. These complexes are useful for therapeutic purposes and experimental purposes. They can also be used as reseants for the treatment of diseases including autoimmune diseases, immunodeficiency diseases,
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                                                                                                                                                                                                                                                                               Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1013 BP; 220 A; 272 C; 327 G; 192 T; 0 U; 2 Other;
(NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 65; 94pp; English.
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                                                                          Marrack P;
                                                                                                                                                             WPI; 1995-320543/41.
P-PSDB; AAR82538.
                                                                          Kappler JW,
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The invention relates to a novel class II major histocompatibility complex (MHC) antigenic peptide composite comprising a peptide containing the T-cell antigenic determinant of a mucous membrane invasive protein and the extracellular region of a class II MHC molecule or at least part of the extracellular region of the class II MHC molecule having an amino acid sequence comprising on or more deletions, substitutions or a matigen-specific comprising of the invention may be useful for detecting an antigen-specific CD4+ T-cell by flow cytometry and for presenting a microcoganism derived mucous membrane invasive protein as an antigen. The method of the invention enables efficient detection of antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence is that of the class II major histocompatibility complex-related I-hablentidna coli heat-labile toxin B subunit (ITB)-leucine zipper (LZ)-BirA fusion cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide-Class II major histocompatibility complex (MHC) composite, useful for detecting antigen specific CD4+ T-cell, comprises antigen peptide containing epitope of mucous membrane invasive protein, and extracellular region of MHC.
                                                                                                                                                        825
646 ATGGCCAGGAGGAGGAGGGGGGCTCTCATCCACACACATATTAGGAATGGGGACTGGA 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "I-Ab(beta)-Escherichia coli heat-labile toxin
B subunit (LTB)-leucine zipper (LZ)-BirA fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            class II major histocompatibility complex; MHC; CD4+ T-cell detection; flow cytometry; mucous membrane invasive antigen; I-Ab(beta)-heat-labile toxin B subunit-leucine zipper-BirA fusion; LTB;
                                                                                                                                         ATGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         I-Ab(beta)-E. coli heat-labile toxin B subunit-LZ-BirA fusion cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .915
                                                                                                                                                                                                                                                                                                                                      ADQ31228 standard; cDNA; 915 BP.
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                                                                                                                                               Gape
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                                                                                                                                               9
                                                                       DB 12; Length 915;
A; 242 C; 271 G; 174 T; 0 U; 0 Other;
                                                                ery Match 66.1%; Score 628.6; DB 12; Length st Local Similarity 91.9%; Pred. No. 1.3e-136; tches 677; Conservative 0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT86989 standard; DNA; 1382 BP.
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Sequence 915 BP; 228
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Single chain major histocompatibility complex comprising linked alpha and beta chains - useful for suppressing an immune response to an auto:Immune disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.9%; Score 607.8; DB 2; Length 1382; Best Local Similarity 89.6%; Pred. No. 1e-131; Matches 673; Conservative 0; Mismatches 57; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                          Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                     The present sequence was used in the construction of major histocompatibility complex (MHC) fusion complexes
                                                                                                                                                                                           Wong HC;
                                                                                                                                                                                                                                                                                                                Example 17; Page 140-141; 217pp; English.
                    Location/Qualifiers
6. .1382
/*tag= a
                                                                                                                                                                                           Rhode PR, Jiao J, Burkhardt M,
                                                                                                                    97WO-US001617
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                                                                                                                                                                    (DADE-) DADE INT INC
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                                                                                                                                            31-JAN-1996;
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                                                                     W09728191-A1
                                                                                             07-AUG-1997
Synthetic.
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                        GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG
                                                                                                ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
                                                                                                                                                    585 ACAGTGGGGGTCTCATCCACACACGCTTATTAGGAATGGGGGACTTGCCAGGTCCTG
                                                                                                                                                                                                                                    645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC
                                                                                                                                                                                                      GTCATGCTGGAGATGACCCCTCATCAGGAGAGGTCTACACCTGCCATGTGGAGCATCCC
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WPI; 2003-341126/32. P-PSDB; ABU72108. Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis, allergies.

Rhode PR, Weidanz JA, Grammer S, Edwards AC;

Chavaillaz P, Jiao JJJ;

Wong HC,

(DADE-) DADE INT INC.

94US-00283302. 95US-00382454. 97US-00776084.

29-JUL-1994; 01-FEB-1995; 17-JAN-1997; Example 17; Fig 29; 126pp; English.

The invention relates to a major histocompatibility complex (MHC) fusion complex (I) comprising an MHC molecule that contains a peptide-binding groove, and a presenting peptide covalently (e.g. an antigent peptide) linked to the MHC molecule, where (I) is capable of modulating the activity of a T cell. Also included are a DNA construct coding for the complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-As or human HLA-ABI, human leukocyte antigen-DRI), a multivalent MHC fusion complex comprising two or more linked complexes, identifying a peptide that can modulate the activity of T cells (involving introducing into host cells cloning vectors that each contain the fusion complex DNA, culturing the host cells under conditions suitable for expression of the MHC fusion complex, and selecting host cells that express MHC fusion

complex that modulate the activity of T cells), a single recombinant expression vector comprising DNA that codes for the alpha and beta chains of the fusion complex MHC protein, a single recombinant expression vector comprising DNA that codes for a T cell costimulatory factor and the alpha and beta chains of the MHC fusion complex. The DNA constructs can contain the expression of the fusion complex. Also included are inducing an immune cresponse in a mammal (including vaccinating a mammal against a targeted disorder, by administering DNA sequence comprising a fusion complex, or DNA sequence coding for a fusion complex which is a single chain fusion at the contains a transmembrane domain, and a presenting peptide that is a T cell receptor (TCR) antagonist or partial agonist and is covalently linked to the MHC protein, or DNA sequence complex which is a single chain fusion molecule. The methods are useful for identifying a peptide that can modulate the cativity of T cells, inducing an immune response in a mammal disorder culculumnant response in a mammal. The disorders include an autorimmune disorder such as multiple sclerosis, insulin-dependent disbetes mellitus, rhemmatoid arthritis, mysathenia gravis or chronic allergies. The present contains a mouse MHC class II I-Ad fusion complex of the ä 81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140 105 gerécreacedréanateancéanécrésicérécracegnéseségeségnadeségeségn 164 165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACACCAAC 224 320 440 560 561 GTGACAGATTTCTACCCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 620 66 AGCAGCCCAAGGAC-------CTTAAGTATCTCTCAGGCTGTTCAC 104 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 260 225 GGGACGCACATACGCCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGGCGGCCAGACGCCGAG 380 344 404 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGCTTGAACAGCCCCAAT 500 464 524 680 525 greacagarricracceaeceaagarcaaagreeceregricaggarreeceagaggag 584 21 ATGGCTCTGCAGATCCCCGGCCTCCTCTCAGCTGCTGGGTGGTGGTGGTGCTGTGCTG 285 TACGACAGCGACGTGGGGGGAGTACCGCGGGGGACCTGGGGCGGCCAGACGCCGAG 405 AGACACAACTACGAGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT GTCGCCATCTCCCTGTCCCAGGACAGACGCCCTCAACCACCACAACACTCTGGTCTGTTCG ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGCCGTGC GTCGCCATCTCCCTGTCCAGGACAGAGCCCTCAACCACACAACACTCTGGTCTGTTCG 141 ATCGTGGTGTCCGGCAGCTGGGACGGAGGTGGGGGCTCACTAGTGCCCCCGAGGCTCTGGA Сарв Pred. No. 1e-131; 0; Mismatches 57; Indels 21; Score 607.8; DB 8; Length 1382; Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other; Match 63.9%; Local Similarity 89.6%; Hes 673; Conservative C invention 261 321 381 441 465 Query Match 201 501 621 Matches 셤 셤 셤 g 셤 셤 셤 ò g 셤 ઠે 유 ଚ δ ઠે ò ŝ ઠે δ ò ઠે

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165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCCAAC
                                                                                                                                                                                                         GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG
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95US-00382454.
97US-00776084.
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01-FEB-1995;
17-JAN-1997;
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                                                                         645 GTCATGCTGGAGATGACCCCTCATCAGGGAGATCTACACCTGCCATGTGGAGCATCCC 704
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       585 ACAGTGGGGGTCTCATCCACACACTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Construction, major histocompatibility complex, MHC, fusion complex; SSC1 single chain gene; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence was used in the construction of major histocompatibility complex (MHC) fusion complexes
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Pred. No. 1e-131;
0; Mismatches 57;
                                                                                                                                            741 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 771
                                                                                                                                                                   705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
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P-PSDB; AAW29212.
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225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284

Jiao JJJ Chavaillaz P,

WPI; 2003-341126/32. P-PSDB; ABU72106.

Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis, allergies.

Example 17; Fig 27; 126pp; English.

The invention relates to a major histocompatibility complex (WHC) fusion complex (I) comprising an WHC molecule that contains a peptide-binding groove, and a presenting an WHC molecule that contains a peptide-binding groove, and a presenting peptide covalently (e.g. an antigenic peptide) linked to the WHC molecule, where (I) is capable of modulating the complex, where the WHC molecule is a class II WHC (e.g. mouse I-Ad or I-As, or human HLA-DR1 (human leukocyte antigen-DR1), a multivalent MHC fusion complex, omprising two or more linked complexes, identifying a peptide that can modulate the activity of T cells (linvolving introducing into host cells condition the fusion complex DR1, culturing the host cells under conditions suitable for expression of the Complex that modulate the activity of T cells), a single recombinant expression of the fusion complex, and selecting host cells, a single recombinant expression of the fusion complex MHC protein, a single recombinant expression of the fusion complex MHC protein, a single recombinant expression of the fusion complex. Also included are inducing an immune beta chains of the MHC fusion complex. The DNA constructs can contain hererologous leader peptide sequences and Kozak sequence for efficient expression of the fusion complex. Also included are inducing an immune response in a mammal (including vaccinating a mammal length MHC molecule that contains a transmembrate domain, and a presenting peptide that is a T cell receptor (TCR) antagonist or partial agonist and is covalently linked to the MHC protein, or DNA sequence coding for the fusion complex which is a single chain fusion of the mammal dincing a peptide that is a T cell receptore (TCR) antagonist or partial agonist and is covalently linked to the MHC protein, or DNA sequence coding for the fusion complex which is a single chain fusion or complex which is a single receptor or partial agonist and a mammal. The disorder is an autoimmune disorder. The mammal against a targeted disorder; mammal against a targeted nvention

Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;

200 81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140 66 AGCAGCCCAAGGAC---------CTTAAGTATCTCTCAGGCTGTTCAC 104 80 65 6 ATGGCTCTGCAGATCCCCCAGCCTCCTCTCAGCTGCTGGTGGTGCTGATGGTGCTG 141 ATCGTGGTGCGGCAGCTGGACGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 21 ATGGCTCTGCAGATCCCCAGCCTCCTCTCAGCTGCTGTGGTGGTGGTGGTGGTG Score 607.8; DB 8; Length 1385; Pred. No. 16-131; 0; Mismatches 57; Indels 21; nery Match 63.9%; set Local Similarity 89.6%; tches 673; Conservative

201 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACAAC 260

105 genéencaceendaaancaaceaaeeneeneenaecegaaeeegaaeeegaaeeegaa

165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACAAC

GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC

261

164

320

224

Single chain major histocompatibility complex comprising linked alpha and beta chains - useful for suppressing an immune response to an auto:immune disease, e-g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, etc. 500 560 524 620 584 680 644 740 321 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 380 404 464 285 TACGACACGACGTGGGGGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGGGCTGC AGACACAACTACGAGGGCCGGAGACCAGCTCCCTGCGGGCGCGCTTGAACAGCCCAAT GTCGCCATCTCCCTGTCCAGGACAGAGCCCTCAACCACCACAAAACTCTGTCG 585 ACAGTGGGGGTCTCATCCACACATATTAGGAATGGGGACTGGACCTTCCAGGTCCTG GTCATGCTGGAGATGACCCCTCATCAGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 381 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAAACGCGGGCCGAGGTGGACACGGCGTGC 405 agacacaacraccaegegecegagaccaecaccaecerecegecegecrasaacaeceaar 465 GTCGCCATCTCCCTGTCCAGGACAGAGCCCTCAACCACCACAACACTCTGGTCTGGTCG GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG ACAGTGGGGGTCTCATCCACACACTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG GTCATGCTGGAGATGACCCCTCATCAGGAGAGGTCTACACCTGCCATGTGGAGCATCCC major histocompatibility complex; MHC; fusion complex; 705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735 741 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 771 Wong Location/Qualifiers 6. .1508 /*tag= a Jiao J, Burkhardt M, 97WO-US001617. AAT86988 standard; DNA; 1508 96US-00596387 Construction, major histoco SCT1 single chain gene; ss. 27-MAR-1998 (first entry) SCT1 single chain gene. (DADE-) DADE INT INC. WPI; 1997-402555/37. P-PSDB; AAW29213 WO9728191-A1. 30-JAN-1997; 31-JAN-1996; 07-AUG-1997. Rhode PR, Synthetic. 441 645 AAT86988; 501 561 621 681 g 유 g a q g ઠે Š 셤 ઠે 8 ઠે ઠે 셤 8

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                                                                                                   ery Match 63.9%; Score 607.8; DB 2; Length 1508; st Local Similarity 89.6%; Pred. No. 1.1e-131; tches 673; Conservative 0; Mismatches 57; Indels 21;
                                                                             Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;
                                      The present sequence was used in the construction of major histocompatibility complex (MHC) fusion complexes
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               Example 17; Page 137-139; 217pp; English.
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The invention relates to new single chain major histocompatibility complex (sc-MHC) class II complexes that comprise a peptide binding groove, and a modified class II beta 2 chain or covalantly linked immunoquobulin (Ig) light chain constant (CI) region. The MHC complexes are useful for detection and analysis of peptide ligands, pathogenic Tecals, for functional, cellular and molecular assays. They can be used to identify and isolate T cell receptor and/or MHC agonists and antagonists. They can also be used to calls involved in immune-related disorders. They can also be used to raise antibodies and to screen immune cells. It is also use in a method of suppressing an immune response in mammals. The sc-MHC complexes of comprising modified class II beta 2 chains and/or Ig-C1 regions are soluble and provide enhanced yield. These MHC complexes also can contain single antigenic peptides readily isolated from expressing cells in significant quantities. The polyspecific MHC complexes also provide a means to detect cells expressing multiple target structures with a single complex. The present sequence represents a DNA encoding a single chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single chain major histocompatibility complex class I complexes
Major histocompatibility complex; MHC; single chain MHC; sc-MHC peptide binding groove; immunoglobulin; T cell receptor; immune immune-related disorder; antigenic peptide; fusion protein; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhode PR, Acevedo J, Burkhardt M, Jiao J, Wong HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 1; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                         98WO-US021520.
                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00960190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUNO-) SUNOL MOLECULAR CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-418411/35.
P-PSDB; AAY27111.
                                                                                                                                                                                                                                                                                                                                                         13-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-1997;
                                                                                                                                                                                                                  WO9921572-A1
                                                                                                                                                                                                                                                                                       06-MAY-1999
                                                                                                                                                 Synthetic.
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BP

AAX89069 standard; DNA; 1508

14-SEP-1999 (first entry)

AAX89069

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                                                                                                         345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGCGTGC
                                                                                                                                                                                                                                                                                                                       465 GTCGCCATCTCCCTGTCCAGGACAGAGCCCTCAACCACCACCACCACCACTCTGGTCTGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                    ACAGTGGGGGTCTCCACCACCACTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    585 ACAGIGGGGTCTCATCCACACATATTAGGAAIGGGGACTGGACCTTCAGGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCATGCTGGAGATGACCCCTCATCAGGGAGGGTCTACACCTGCCATGTGGAGCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC
                                                                        381 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC
                                                                                                                                                                         441 AGACACAACTACGAGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT
                                                                                                                                                                                                                                                                                                                                                                        GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCCAGGAGGAG
                                                                                                                                                                                                                     405 acacacaacraccadeccedadaccaccaccaccaccaccacacaccacacaccaar
                                                                                                                                                                                                                                                                         MHC; major histocompatibility complex; gene therapy, fusion complex; peptide-binding groove; T cell modulation; class II MHC; vaccine; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes mellitus; myasthenia gravis; immunogen; chronic allergy; mouse; ds; I-Ad; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edwards AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse MHC I-Ad/Ova 323-339 synthetic gene SCT1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           741 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACA60743 standard; DNA; 1508 BP
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95US-00382454.
97US-00776084.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUN-2003 (first entry)
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P-PSDB; ABU72107.
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01-FEB-1995;
17-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-DEC-2002
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                                                                                                                                                                                                                                                                         501
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The invention relates to a major histocompatibility complex (WHC) fusion complex (I) comprising an MHC molecule that contains a peptide-binding groove, and a presenting peptide covalently (e.g. an antiganic peptide) inked to the MHC molecule, where (I) is capable of modulating the tent of inked to the MHC molecule, where (I) is capable of modulating the tent of complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I complex complex complex complex or more linked complexed, identifying a peptide that can modulate the activity of T cells (involving introducing culturing the host cells under conditions suitable for expression of the Complex that modulate the activity of T cells), a single recombinant complex that modulate the activity of T cells), a single recombinant complex that codes for a T cell cost.mulacory factor and the alpha complex that codes for a T cell cost.mulacory factor and the alpha complex that codes for a T cell cost.mulacory factor and the alpha complex that codes for a T cell cost.mulacory factor and the alpha complex that codes for a T cell cost.mulacory factor and the alpha complex that codes for a T cell cost.mulacory factor and the alpha complex that codes for a T cell cost.mulacory factor and the alpha complex that codes for a finding vaccinating a nammal again or complex, or compression of the fusion complex. Also included are inducing a fusion complex, or ceptone in a mammal (including vaccinating a mammal identifying a peptide that contains a transmembrates domain, and confined to the mammal a DNA sequence comprishing an examement of the mammal and including an information or DNA sequence coding for the fusion complex which is a single chain fusion complex which is a single chain fusion complex of the mammal against a targeted disorder, and multiple solerosi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGGTCGCTGGAGCACCCG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 gcrecrcacecreaaancaaceaaecreerecraeceaaeeeeceeaaaeeeceees
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 ATGGCTCTGCAGATCCCCAGCCTCCTCTCAGCTGCTGTGGTGGTGGTGGTGGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;
                   Sxample 17; Fig 28; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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Example 17; Fig 29; 210pp; English.
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                                                     /*tag= j
/note= "EE tag"
                                                                                                                                  95WO-US009816
                                                                                                                                                       94US-00283302.
                                                                                                                                                                                                            Wong HC, Rhode PR, We
Chavaillaz P, Jiao J;
                                                                                                                                                                                       (DADE-) DADE INT INC.
                                                                                                                                                                                                                                             WPI; 1996-129343/13.
P-PSDB; AAR98907.
                                                                                                                                   31-JUL-1995;
misc_feature
                                                                                                                                                       29-JUL-1994;
01-FEB-1995;
                                         misc_feature
                                                                                       WO9604314-A1
                                                                                                             15-FEB-1996.
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                                                                                                                                                                                                             704
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/*tag= b
//label= I-Ad beta chain leader
/note= "murine MHC class II I-Ad gene beta chain leader
                                                                                                                                                                                                                                                                                                                                                                                                     MHC; major histocompatibility complex; PCR; polymerase chain reaction; T cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheusin-dependent gravis; ds.
                                                                                                                                                                                                      ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= h
/label= I-Ad_alpha1
/note= "murine MHC class II I-Ad gene alpha-2 domain"
                                  AGACACACTACGAGGGCCGGAGACCAGCACCTCCCTGCGGCGCGCTTGAACAGCCAAT
                                                       GTCGCCATCTCCCTGTCCAGGACAGACGCCCTCAACCACCACAACACTCTGGTTCG
                                                                                                  GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG
                                                                                                                                             ACAGTGGGGGTCTCATCCACACACATTAGGAATGGGGACTGGACTTCCAGGTCCTG
                                                                                                                                                                                        GTCATGCTGGAGATGACCCCTCATCAGGAGGAGGTCTACACCTGCCATGTGGAGCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= e
/labcl= I-Ad_betal
hotc== murine MHC class II I-Ad gene beta-1 domain"
453. .?34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene beta-2 domain"
                                                                                                                                                                                                                                                                                                                                                                                 Vector SCE1-derived single chain gene encoding MHC fusion complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= c
/label= OVA 323-339
/note= "chicken ovalbumin residues 323-339"
138. 167
/rtag= "10 residue linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= g
/note= "24 residue peptide linker"
807. .1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= I-Ad_beta2
/note= "murine WHC class II I-Ad
735. .806
                                                                                                                                                                                                                                    771
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                                                                                                                                                                                                                                      741 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
6. .1382
/*tag= a
                                                                                                                                                                                                                                                                                                                 AAT17588 standard; DNA; 1382 BP
                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                               465
                                                                                                     561
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                                                                                                                                                621
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AAT17588 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SCEI. The MHC fusion complex comprises at least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a transmembrane domain. DNA encoding a MHC fusion complex may be cloned transmembrane domain. DNA encoding a MHC fusion complex may be cloned controlly. DNA encoding a MHC fusion complex or a single chain fusion activity. DNA encoding a MHC fusion complex or a single chain fusion complexes may be used to suppress an immune response in an animal suffering from an immune disorder e.g. multiple sclerosis, insuling chronic allergies. The complexes may also be used in the treatment of chronic allergies. The complexes may also be used in the treatment of chronic allergies. The complexes may also be used in the treatment of chronic allergies. The complexes may also be used in the treatment of chronic allergies and dogs. The MHC fusion complexes can be produced such that they contain a single antigenic peptide including one of known structure, additionally a wide range of peptides can be contain a single antigenic peptide including one content that they contain a single antigenic peptide including one content that they contain a single antigenic peptide including one content that they contain a single antigenic peptide can be contain a single antigenic peptide including one contain a single antigenic peptides can be contain a single and complexes and c
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/*teg= i
/labba I-Ad_alpha2
/note= "murine MHC class II I-Ad gene alpha-2 domain"
1353. .1379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1382 BP; 320 A; 374 C; 404 G; 284 T; 0 U; 0 Other;
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gene alpha-2 domain"

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AAT17586 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SSC1. The MHC fusion complex comprises at least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a transmembrane domain. DNA encoding a MHC fusion complex may be cloned into a host cell to express the complex. The transformed cells may then complex to the used to identify peptides that modulate, pref. antegonise, T cell activity. DNA encoding a MHC fusion complex or a single chain fusion complexes may be used to suppress an immune response in an animal suffering from an immune disorder e.g. multiple sclerosis, insulin chapendent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or chronic allergies. The complexes may also be used in the treatment of chronic allergies. The complexes may also be used in the treatment of chronic allergies. The complexes may also be used in the treatment of chronic allergies. The complexes may also be used in the treatment of chronic allergies, and additionally a wide range of peptides can be produced such that they contain a single antigenic peptide including one of produced for T cell interaction
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                                                                                                                   /*tag= h
/label= I-Ad_alphal
/note= "murine MHC class II I-Ad gene alpha-2 domain"
1068. .1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Major histocompatability complex fusion complex for modulating T cell activity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.
/label= I-Ad_beta2
/note= "murine MHC class II I-Ad gene beta-2 domain"
/35. .806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1385 BP; 316 A; 384 C; 398 G; 287 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grammer S, Edwards AC;
                                          /*tag= g
/note= "24 residue peptide linker"
107. .1067
                                                                                                                                                                                                                                         class II I-Ad
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/label= I-Ad_alpha2
/note= "murine MHC cl
1353. 1382
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/note= "6xHis tag"
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Chavaillaz P, Jiao J;
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                                              285 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTCGGGCCGCGAGACGCCGAGA
                                                                                                                                             345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGGGTGC 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284
                                                                                                                         381 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGGCCGAGGTGGACACGGCGTGC 440
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/label= I-Ad_beta_chain_leader
/note= "murine MHC class II I-Ad gene beta chain leader
sequence"
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                                                                                                                                                                                                    441 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGCGTTGAACAGCCCAAT
                                                                                                                                                                                                                                                                                                       561 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGAG
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/label= I-Ad betal
/note= "murine MHC class II I-Ad gene beta-1 domain"
453. 734
/*tag= f
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label= OVA 323-339
note= "chicken ovalbumin residues 323-339"
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/note= "10 residue linker peptide"
168. .452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 771
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380
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645 Greargergaagargaccercarcagaagagarcracaccraccargrasagarcce 704
                                                                                                                                                                                                          GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6..86
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/|note= "murine MHC class II I-Ad gene beta_chain_leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHC; major histocompatibility complex; PCR; polymerase chain reaction; T cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myasthenia gravis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCGGCTTGAACAGCCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585 ACAGTGGGGGTCTCATCCACACATATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
                                                                                                   TACGACAGGACGTGGCCGAGTACCGCGCGGTGACCGAGCTGGGCGCCGAGACGCCGAG
                                                                                                                                                                                                                                                                                                                                                                               345 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGACGGCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG
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                                                                          GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC
                                                                                                                                                                 GGGACGCAGGCGATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC
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/label= OVA 323-339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
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6. .1508
/*tag= a
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87. .137
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AAT17587 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SCT1. The MHC fusion complex comprises at least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a cramsmembrane domain. DNA encoding a MHC fusion complex may be cloned transmembrane domain. DNA encoding a MHC fusion complex may be cloned controlled to express the complex. The transformed cells may then complex of a single chain fusion activity. DNA encoding a MHC fusion complex or a single chain fusion complexes may be used to suppress an immune response in an animal suffering from an immune disorder e.g. multiple sclerosis, insulin chaptened mallitus, rheumatcoid arthritis, myasthenia gravis or chronic allergies. The complexes may also be used in the treatment of chronic allergies. The complexes may also be used in the treatment of produced such that they contain a single antigenic peptide including one of known structure, additionally a wide range of peptides can be contain a single antigenic peptide including one contain a single antigenic peptide can be contained for T cell interaction
                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= j
/lobel= I-Ad_alpha-TM
/noe= "murine MHC class II I-Ad gene alpha-transmembrane
domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Major histocompatability complex fusion complex for modulating T cell activity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.
                                                                                                                                                                                                                                                            /*tag= h
/label= I-Ad alpha!
/note= "murine MHC class II I-Ad gene alpha-2 domain"
1068. .1352
                                                                                                                                                                                                                                                                                                                                  /*tag= i
/labol= n-Ad_alpha2
/labol= "murine MHC class II I-Ad gene alpha-2 domain"
1353. .1505
                                                                 /*tag= e
//label= I-Ad_betal
/note= "murine MHC class II I-Ad gene beta-1 domain"
453. .734
                                                                                                                                                                      domain,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wong HC, Rhode PR, Weidanz JA, Grammer S, Edwards AC;
Chavaillaz P, Jiao J;
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/note= "murine MHC class II I-Ad gene bet
735. 806
/*tag= g
/note= "24 residue peptide linker"
807. .1067

    167
    tag= d
    note= "10 residue linker peptide"

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89.5%;
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95US-00382454
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Best Local Similarity
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01-FEB-1995;
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141 ATCGTGGTGTCCGGCAGCTGGACGGAGGTGGGGGCTCACTAGTGCCCCCGAGGCTCTGGA 200
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                                                                                                  81 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 140
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                                               165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGGGAGTGCTACTACACCCAAC
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itches 672; Conservative
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Aavi2068 Murine IA
Aacto4269 Hubrid IA
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Aact0746 Wector SC
Aat66989 SCEI sing
Aca60744 Wouse MHC
Aat17586 Wector SC
Aat86986 SCTI sing
Aca60742 Wouse MHC
Aat17597 Wector SC
Aat86988 SCTI sing
Aax89069 SINGle ch
Aax89069 SINGle ch
Aax89069 Novel cel
Adj75986 Marker ge
Adj75986 Marker ge
Adj76989 Murine pC
Abj99019 Murine pC
Abj99019 Murine pC
Abj99019 Murine pC
Abj99019 Murine pC
Aat6520 Mouse I-A
Aat6520 Mouse I-A
Aat6901 IAS MBP 1-14
Abj99021 IAS MBP 1-14
Abj99021 IAS MBP 1-14
Abj99021 IAS MBP 9
Abj99021 IAS MBP 9
Abj99031 IAS MBP 9
Abj99032 DNA encod
Acc4482 Lung canc
Adc3751 Human maj
Ad6315 Toxicity-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin; major histocompatibility complex; Fc region; antigen; T lymphocyte; immunostimulant; vaccine; infection; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding a fusion protein comprising a beta chain of MHC.
                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                   AAT86989
ACA60744
AAT1.7586
AAT1.7587
ACA60742
AAT1.7587
AAT1.869
AAX89069
AAX89069
AAX89069
AAX89069
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ABI99038
AAD03170
AAT06286
AAA056286
AAA056286
AAA035055
ABI99031
ABI99032
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AAT60705
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF55099 Btandard; DNA; 921
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WO200109194-A1
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1219
1161.5
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   Aaf55099 DNA encod
Aat04262 Hybrid IA
Adg31225 I-Ab(beta
                                                                May 31, 2006, 23:04:55 ; Search time 714 Seconds (without alignments) 4482.160 Million cell updates/sec
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1620
1 MALQIPSLLLSAAVVVLMVL......LKWKLQALKKKLAQHHHHHH 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                10489840
           GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                               nucleic search, using frame_plus_p2n model
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Match Length
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100.0 77.5 76.2

1620 1255.5 1235

Score

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(CNRS ) CNRS CENT NAT RECH SCI.
Glaichenhaus N, Malherbe L;
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WPI; 2001-182944/18. P-PSDB; AAB67481. New soluble recombinant protein, useful e.g. as immunostimulant, comprises dimeric major histocompatibility complex molecule fused to immunoglobulin Rc region.

Example 1; Page 34-35; 43pp; French.

The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the Fc region of an immunoglobulin. The recombinant proteins, when linked to an antigenied, sate used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Ag-reactive T cells from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising a beta chain of MHC molecules

Sequence 921 BP; 214 A; 265 C; 286 G; 156 T; 0 U; 0 Other;

	921	306	0	0	0	0
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	6.68e-144	1620.00	100.04	100.04	100.04	S
nment Scores:	. No.:		ent Similarity:	Local Similarity:	y Match:	

0-048-116B-6 (1-306) x AAF55099 (1-921)

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21		40
61		120
41	11eValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly	09
121		180
19	GlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrThrAsn	80
181	GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC	240
81	GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg	100
241	GGGACGCAGCGCATACGGCTCGTGATACATCTACAACCGGGAGGAGGAGTACGTGCGC	300
101		120
301	TACGACGACGTGGGGGGGTACCGCGGGGGGCCGAGCCGGGCCGGCC	360
121		140
361	TACTGGAACAGCCAGCCGGGGGTCTCCTGGAGCGAACGCGGGGCCGAGGTGGACACGGCGTGC	420
141	ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGluBroAsn	160
421	AGACACCAGCGGGGGCCGGAGACCAGCCCCCCGGCGCGCGCTTGAACCAGCCCAAT	480

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complement(158. .212)
/hag= # /note= "primer #332 binding site"
complement(199. .250)
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                                                                                                                                                                                                                                                                                                                                                             /*teg= g
//note= "primer #333 (see AAT04263) binding site"
371.389
                                                                                                                                                                                                                                                                                                            Polymerase chain reaction; PCR; primer; amplify; major histocompatability complex; MRC; T-cell receptor; TCR; autoimmune disease; immunodeficiency disease; immune response; immunoproliferation disease; graft-host rejection; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                               61. .828
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61. .141
/ttag= d
/note= "leader region"
complement(119. .172)
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                                                                                                                                                                                                                                                                   AAT04262;
                                                                                                                                                                                                                                                                                                                                                 Synthetic
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Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.
                                                                                          / regs 1
/notes "probable primer binding site (primer #271)"
532. :554
/*tags k
/notes "probable primer binding site (primer #272)"
108. :836
== "probable primer binding site (primer #270)". 825
                                                                                                                                                                                                                              /*tag= 1
/note= "probable primer binding site (primer #259)"
877. .893
                                                                                                                                                                                                                                                                                             /*tag= m
/note= "probable primer binding site (primer #232)"
                                                              product= "IA beta chain beta 2 region"
21. .550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 53; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                           95WO-US002689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00207481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marrack P;
      note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-320543/41.
P-PSDB; AAR82533.
                                                                                                                                                                                                                                                                                                                                                           WO9523814-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAR-1994;
                                                                               primer_bind
                         mat_peptide
                                                                                                                                              primer_bind
                                                                                                                                                                                                             primer_bind
                                                                                                                                                                                                                                                                         primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                    08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kappler JW,
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This sequence represents a hybrid IA beta chain gene, containing the chicken ovalbumin peptide (cOVA). This sequence was used in the construction of a hybrid IA alpha beta dimer. The encoded protein (plAd-OVA) was found to be more stable than the IA alpha beta dimer. The stability was decreased by the addition of a MHC groove specific binding peptide (e.g. see AAR82527, AAR82528 and AAR82531), compared to an increase seen on the addition of a MHC binding peptide to IE k/d-MC.

These complexes may be used to regulate an immune response. The complexes are capable of being recognised by a TCR alone or in combination with additional MHC proteins. These complexes are useful for theraputic purposes and experimental purposes. They can also be used as reagents for the treatment of diseases including autoimmune diseases, immunodeficiency diseases, immunoproliferation diseases, and graft-host rejection

Seguence 893 BP; 204 A; 239 C; 275 G; 175 T; 0 U; 0 Other;

	893	242	ø	7	Ŋ	-4
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	2.39e-109	1255.50	95.48	93.1\$	77.5\$	~
inment Scores:	i. No.:		sent Similarity:	: Local Similarity:	.y Match:	•

[0-048-116B-6 (1-306) x AAT04262 (1-893)

- 21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro

03-DEC-2003; 2003JP-00404367

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121 TyrTrpasnSerGlnProGluileLeuGluArgThrArgAlaGluValAspThrAlaCys 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          765
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                                                                                                100
                                                                                                                                               TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            class II major histocompatibility complex; MHC; CD4+ T-cell detection; flow cytometry; mucous membrane invasive antigen;
I-Ab(beta)-cholera toxin B subunit-leucine zipper-BirA fusion; CTB; 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                706 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGTCTACACCTGCCATGTGGAGGATCCC
              346 TACGACAGCGACGTGGGCGAGTACCGCGGGGGACCGAGCCGGCGGCGGCCAGACCCGAG
                                                                                                                                                                                                                  406 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGCGTGC
                                                                                                                                                                                                                                                 141 ArghisantyrGluGlyProGluthrSerThrSerTeuArgArgLeuGluGlnProAsn
                                                                                                                                                                                                                                                                  466 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGCGCTTGAACAGCCCAAT
                                                                                                                                                                                                                                                                                               ValAlalleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer
                                                                                                                                                                                                                                                                                                                                                   ValThraspPheTyrProAlaLyslleLysValArgTrpPheArgAsnGlyGlnGluGlu
                                                61 GlyGlyGlyGerGluArgHisPheValValGlnPheLy6GlyGluCy8TyrTyrThrAsn
                                                                                                 GlyThrGlnArgleArgleuValThrArgTyrIleTyrAsnArgGluGluTyrValArg
                                                                                                                                                                                                                                                                                                                          586 greacagarricracccaccaagarcaagrecccrecrecrecagaarceccageage
                                                                                                                                                                                                                                                                                                                                                                                                    ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu
41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "I-Ab(beta)-Cholera toxin B subunit (CTB)-
leucine zipper (LZ)-BirA fusion cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ31225 standard; cDNA; 945 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-2004.
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(SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK
03-DEC-2002; 2002JP-00351818
                                                                                                                    2004-546819/53.
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P-PSDB; ADQ31224

Peptide-Class II major histocompatibility complex (MHC) composite, useful for detecting antigen specific CD4+ T-cell, comprises antigen peptide containing epitope of mucous membrane invasive protein, and extracellular region of MHC.

Example 1; SEQ ID NO 10; 30pp; Japanese.

The invention relates to a novel class II major histocompatibility complex (WHC) antigenic determinant of a mucous membrane invasive protein and the T-cell antigenic determinant of a mucous membrane invasive protein and the extracellular region of a class II MHC molecule or at least part of the extracellular region of the class II MHC molecule having an amino acid sequence comprising one or more deletions, substitutions on additions. The molecule of the invention may be useful for detecting an antigen-specific CD4+ T-cell by flow cytometry and for presenting a microorganism-derived mucous membrane invasive protein as an antigen. The method of the invention enables efficient detection of antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence is that of the class II major histocompatibility complex-related I-Ab(alpha)-Cholera toxiocons of the invention.

Sequence 945 BP; 230 A; 256 C; 294 G; 165 T; 0 U; 0 Other;

	945	244	14	42	4	3
	Length:	Matches:	Conservative:	Mismatches:	Indela:	Gaps:
	2.27e-107	1235.00	84.9%	80.34	76.2	12
nment Scores:	. No. :		ent Similarity:	Local Similarity:	y Match:	

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                                                                                                                                                                                                                                                       124 gcgarcococcarcaccarogcgaacogagciccice---ggrocaggggaagr 180
                                                                                                                                                                                                                                                                                                                           181 GGAGGTGGAGGGTCTGAAAGGCATTTCGTGTACCAGTTCATGGGCGAGTGCTACTTCACC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgFroAspAla 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluTyrTrpAenSerGlnProGluIleLeuGluArgThrArgAlaGluValAepThrAla 139
                                        13
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                                                                                                                                                                                                                                                                                                                                                                                       66
                                                                 ::: |||:::::|||
4 GTGTCTGAAGCTCCCTGGAGGTTCCTACATGGCAAAGCTGACAGTGACACTGATGGTG 63
                                                                                                                         33
                                                                                                                         LeuSerSerProGlyThrGluGlyGlyAsnSerlleCysPheSerProSerLeuGluHis
                                                                                                                                                                                                                                                                                                                                                                                                              CysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnPro
                                        1 MetAlaLeuGlnIlePro---SerLeuLeuLeuSerAlaAlaValValValleuMetVal
                                                                                                                                                                                                               40 ProlleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySer
                                                                                                                                                                                                                                                                                                    GlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrThr
                                                                                                                                                                                                                                                                                                                                                                                          80 AsnGlyThrGlnArglleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrVal
3-048-116B-6 (1-306) x ADQ31225 (1-945)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
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480

Tecagacacaactraceaeeecceeaeacccacaccrccrccreceeeecrreaacaeccc

421

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Peptide-Class II major histocompatibility complex (MHC) composite, useful for detecting antigen specific CD4+ T-cell, comprises antigen peptide containing epitope of mucous membrane invasive protein, and extracellular
                                            199
                                                                                         219
                                                                  9
                                                                                                               99
                                                                                                                                        239
                                                                                                                                                           crosrcardcrosadargaccccrcoscososadadescrarcaccrorcaccardadedra 720
                                                                                                                                                                                  240 ProSerLeulysSerProlleThrValGluTrpArgAlaGlnSerGluSerAlaArgSer 259
                                                                                                                                                                                                 834
                                                                                                                                                                                                                                                                              280 LeulyslyslyskshalaGlnLeulysTrplysleuGlnAlaLeulyslyslysleuAla 299
                                                                                                                                                                                                                                                                                          1.915
/*tag=
/*tag=
//roduct= "I-Ab(beta)-Escherichia coli heat-labile toxin
B subunit (LTB)-leucine zipper (LZ)-BirA fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        class II major histocompatibility complex; MHC; CD4+ T-cell detection; flow cytometry; mucous membrane invasive antigen; I-Ab(beta)-heat-labile toxin B subunit-leucine zipper-BirA fusion; LTB;
                                            SerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGlu
                                                                                                       TCAGTGACAGATTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAG
AsnvalalalleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCys
          LeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHis
                                                                                                                                                                                                                                               GluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnVal
                                                                                                                                                                                                                                   LysGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I-Ab(beta)-E. coli heat-labile toxin B subunit-LZ-BirA fusion cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SENT-) SENTAN KAGAKU GLJUTSU INCUBATION CENT KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-DEC-2003; 2003JP-00404367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-2002; 2002JP-00351818.
                                                                                                                                                                                                                                                                                                                                                                                                  ADQ31228 standard; cDNA; 915
                                                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                           300 GlnHisHisHis 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-546819/53.
P-PSDB; ADQ31227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
Unidentified.
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                                                                     541
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  160
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                                                                                           200
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Example 3; SEQ ID NO 13; 30pp; Japanese.

The invention relates to a novel class II major histocompatibility complex (MHC) antiganic peptide composite comprising a peptide containing the T-cell antigenic determinant of a mucous membrane invasive protein and the extracellular region of a class II MHC molecule or at least part of the extracellular region of the class II MHC molecule having an amino acid sequence comprising one or more deletions, substitutions or additions. The molecule of the invention may be useful for detecting an antigen-specific CD4+ T-cell by flow cytometry and for presenting a microorganism-derived mucous membrane invasive protein as an antigen. The method of the invention enables efficient detection of antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence is that of the class II major histocompatibility complex-related I-bi(alpha)-Escherichia coli hear-labile toxin B subunit (ITB)-leucine zipper (LZ)-BirA fusion cDNA of the invention.

Sequence 915 BP; 228 A; 242 C; 271 G; 174 T; 0 U; 0 Other;

	915	242	16	32	14	ď
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gana.
	7.14e-106	1219.00	84.9%	79.68	75.28	12
inment Scores:	i. No.:	;e:	sent Similarity:	: Local Similarity:	:y Match:	

.0-048-116B-6 (1-306) x ADQ31228 (1-915)

1 MetalaLeuGlnIlePro---SerLeuLeuLeuSerAlaAlaValValValLeuMetVal

19

63

- 20 LeuSerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHis 39
- 40 ProllevalValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySer
- 109 ATGGTTATCATT-----ACATTTAAGGGTGGTGGTGGTTCTTTAGTTCCTAGA-----

156

210

- 79 GlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThr
- 66 80 AsnGlyThrGlnArglleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrVal
- 211 AACGGGACGCAGCGCATACGATATGTGACCAGATACATCTACAACCGGGAGGAGTACGTG 270
- 100 ArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAla 119
- 120 GluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAla 139
- 140 CysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnPro 159
- 391 recadacacaratacoa de de contracer de con 160 AsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCys 179

510

- SerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGlu 199 570 511 TCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAG 180
- 219 GluThrvalGlyvalSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnVal 200

Major histocompatibility class II antigen; MHC class II; T cell; T lymphocyte; Thi; Th2; activation; CD4+; antigen presenting cell; APC; autoimmune disease; diabetes; multiple sclerosis; autoimmune thyroiditis; systemic lupus erythromatosus; mysathenia gravis; Crohn's disease; inflammatory bowel disease; allary; asthma; contact sensitivity; immunotherapy; therapy; IAd beta chain; mouse; ds; circular; cyclic. ProSerLeuLysSerProlleThrValGluTrpArgAlaGlnSerGluSerAlaArgSer 259 299 744 804 864 GAGACGGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTC 630 LeuvalMetLeuGluMetThrProHisGlnGlyGluvalTyrThrCysHisValGluHis LeulyslyslyslysabanAlaGlnLeulysTrpLysLeuGlnAlaLeulyslysLysLysLeuAla LysGlyGlyGlyGerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAla creerrecececesáriccácráchicarcacricacricaciricaaaaaaaaacreease 踞 AAV12068 standard; cDNA; 4724 Murine IAd beta chain cDNA. 08-JUN-1998 (first entry) GlnHisHisHis 303 CAGCTGCATCAT 876 805 AAV12068; 631 240 691 260 745 280 300 865 220 AAV12068 RESULT ઠે 셤 ò ద ઠે 셤 ઠે 임 Š 셤

97WO-US008697. 96US-0018175P. (SCRI) SCRIPPS RES INST. W09746256-A1. 22-MAY-1997; 23-MAY-1996; 11-DEC-1997. Mus

Peterson PA; Webb SR, Wingvist O, Karlsson L, Jackson MR, WPI; 1998-041895/04.

useful Synthetic antigen presenting cell for activating CD4+ T cells - use treat autoimmune disease, e.g. diabetes, multiple sclerosis, Crohn'disease and inflammatory bowel disease, or allergy, e.g. asthma and contact sensitivity.

S

Example 2; Page 94-96; 141pp; English.

This nucleotide sequence comparises a PCR product obtained by amplification of mouse splenocyte cDNA using primers (see AAV12065 and AAV12066) designed for the amplification of IAd beta chain full-length cDNA. IAd alpha chain cDNA (see AAV12067) has been similarly obtained. The IAd sequences were cloned into metallothionein promoter (see AAV12062)-driven vector pRmHa-3 prior to sequencing. Major histocompatibility complex (WHC) class II IAd heterodimers were expressed at the cell surface of transfected Drosophila Schmeider 2 (ATCC CRL 10974) cells. The invention relates to the preparation and use of synthetic antigen presenting matrices, in particular antigen presenting cells such as insect cells that have been transfected to produce MHC

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antigen presenting molecules with one or more accessory molecules. The matrices are used to activate naive CD4+ T cells and to shift the ongoing activation state into a preferred differentiated population of Th1 or Th2 cells. Applications include the treatment of autoimmune disease, e.g. diabetes, multiple sclerosis, autoimmune thyroiditis, systemic lupus erythematosus, myasthenia gravis, Crohn's disease and inflammatory bowel disease, or an allergy, e.g. asthma and contact sensitivity
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Sequence 4724 BP; 1196 A; 1194 C; 1200 G; 1134 T; 0 U; 0 Other;

4724	228	т	-	37	7
Length:	Matches:	Conservative:	Mismatches:	Indel8:	Gabs:
1.85e-99	1161.50	85.8%	85.4	71.7	~
No.:		ant Similarity:	Local Similarity:	/ Match:	
	1.85e-99 Length:	1.85e-99 Length: 1161.50 Matches:	1.85e-99 1161.50 85.8%	1.85e-99 Length: 1161.50 Matches: 85.8% Conservative: 85.4% Mismatches:	1.85e-99 Length: 1161.50 Matches: urity: 85.8* Conservative: nilarity: 85.4* Mismatches: 71.7* Indels:

)-048-116B-6 (1-306) x AAV12068 (1-4724)

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1128
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                                                                                                                                                                                                                                                                                                                                                                                                     768
                                                                                          537
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20
                                                           40
                                                                                                                       9
                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu
                 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro
                                                                                                                                                                                                   ------TCGBAAGGCATTTCGTGGTCCAGTTCAAGGCGAGTGCTACTACACCAAC
                                                                                                                                                                                                                                                                                                                              ValAlaileSerLeuSerArgThrGluAlaLeuAanHisHisAsnThrLeuValCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCATGCTGGAGATGACCCCTCATCAGGAGAGGTCTACACCTGCCATGTGGAGCATCCC
                                                                                                                         41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly
                                                                                                                                                                                     GlyGlyGlyGlcystGluhrgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn
                                                                                                                                                                                                                                                  GlyThrGlnArgileArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg
                                                                                                                                                                                                                                                               TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu
                                                                                                                                                                                                                                                                                                                                                                          TyrTrpAenSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys
                                                                                                                                                                                                                                                                                                                                                                                          TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGACACACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGGGGCTTGAACAGCCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValThrasppheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrvalGlyvalSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAGTGGGGGTCTCCACCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro
                                                                               511 AGCAGCCCAGGGACTGAGGGCGGAAAC------
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                                451
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------GlyGlyGlyGly 264

261

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*tag= b
note= "binding site for primer #362 (see AAT04270)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (see AAT04271)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= h
note= "probable primer binding site (primer #270)"
31. .959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= k
hotc= "probable primer binding site (primer #272)"
823. .865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag= j
note= "probable primer binding site (primer #271)"
44. .568
                                                                                                                                                                                                                                                                                                                                                 cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer binding site (primer #259)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (primer #366)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "probable primer binding site (primer #76)"
complement(40. .74)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #59) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= g
|note= "primer #365 (see AAT04272) binding site"
885. 403
                                                                                                                                                                                                                                                                                                 Major histocompatability complex; MHC; T-cell receptor; TCR; autoimmune disease; immunodeficiency disease; immune response; immunoproliferation disease; graft-host rejection; therapy; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= n
/note= "probable primer binding site (primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product= "IA beta chain beta 2 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= m
/note= "probable primer binding site
0000. .1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= e
/note= "binding site for primer #363
complement(177. .226)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= f
/note= "primer #364 binding site"
complement(212, .266)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/product= "hybrid IA beta chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= d
/note= "leader region"
complement(140. .191)
||| ||||||
ATGTTGAGCGGCATCGGGGGC 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= 1
/note= "probable
342..976
                                                                                                                   BP.
                                                                                                                   1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US002689
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                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                        Hybrid IA beta chain gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     535. .564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63. .959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63. .143
                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                            M12.C3; pM12-IAb-Ea; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9523814-A1
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                                                                                                                                                                                                               16-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
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                                                                                                                                                                   AAT04269;
                                                                                                                      AAT04269
                                                                                           AATO 4269
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AATO 4269
XXX
AATO 4269
XXX
AATO 4269
XXX
AATO 426
XXX
AATO 4269
AATO 42
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255 764

264

704

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6. .86
/ttag= h
/labal= I-Ad beta chain leader
/note= "murine MHC class II I-Ad gene beta chain leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHC; major histocompatibility complex; PCR; polymerase chain reaction; T cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myashenia gravis; ds.
                                                                                                                                                                         236 HisValGluHisProSerLeuLysSerProlleThrValGluTrpArgAlaGlnSerGlu
                                                                 585 ACTCTGGTCTGCTCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGG
                                                196 AsnGlyGlnGluGluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrp
                                                                                                              216 ThrPheGlnValLeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             class II I-Ad gene alpha-2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                               Vector SCE1-derived single chain gene encoding MHC fusion complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       class II I-Ad gene beta-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
/label= OVA 323-339
/note= "chicken ovalbumin residues 323-339"
138. 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "tag= g
note= "24 residue peptide linker"
077...1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= d
/note= "10 residue linker peptide"
                                                                                                                                                                                                                                                                 825 rcheccreaacaacaacarerreaececcarceeeec 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *teg= h
/label= 1.Ad alphal
/note= "murine MHC class II I-Ad
1068. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= f
/label= I-Ad_beta2
/note= "murine WHC class II I-Ad
735. .806
                                                                                                                                                                                                                                  SerAlaArgSerLys-----GlyGlyGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= e
/label= I-Ad betal
/note= "murine MHC c
453. .734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= 1
/label= I-Ad alpha2
/note= "murine MHC cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
6. .1382
/*tag= a
                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "EE tag'
                                                                                                                                                                                                                                                                                                                                 AAT17588 standard; DNA; 1382
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence"
87. .137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168. .452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
/note= '
                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                AAT17588;
                                                                                                                                                                                                                                       256
                                                                                                                                                                                                                                                                                                                  AAT17588
ID AAT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                   RESULT
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                                               δ
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                                                                                                                                     셤
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                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                    This sequence represents a hybrid IA beta chain gene. This sequence contains a fragment of the IB alpha chain (residues 56-73), as well as a linker and cleavage site. This sequence was transfected into a B cell line (M12.3) using plasmid pM12-IAb-Ba. It was found that the encoded sequence was expressed in these cells. Complexes such as this may be used to regulate an immune response. The complexes are capable of being recognised by a TCR alone or in combination with additional MHC proteins. These complexes are useful for therapeutic purposes and experimental purposes. They can also be used as reasquite for the treatment of diseases including autoimmune diseases, immunodeficiency diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 ValAspThrAlaCysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArg 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuGluGlnProAsnValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHsAsn 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 ArgProAspAlaGluTyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGlu 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 ---GGGGGAAGTGGAGGGGGGGGGCGTTTCGTGTACCAGTTCATGGGGGG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 GluGluTyrValArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGly 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 ThrLeuValCysSerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArg 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 AGCAGCCCAGGGACTGAGGGCGGGAGACTCC----GAAGCTAGCTTTGAGGCTCAG 173
                                                                                            Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerSerProGlyThrGluGlyAglyAsnSerIleCysPheSerProSerLeuGluHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 CysTyrTyrThrAsnGlyThrGlnArglleArgLeuValThrArgTyrIleTyrAsnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        465 GTGGACACGCTGTGCAGACACAACTACGAGGCCCGGAGACCCACACCTCCCTGCGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 ProArgGlySerGlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------IleValValSerGlySerTrpAspGlyGlyGlySerLeuVal
                                                                                                                                                                                                                                                                                                                                                                                Sequence 1013 BP; 220 A; 272 C; 327 G; 192 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                   immunoproliferation diseases, and graft-host rejection
                                                                                                                                                                                                                                                                                                                                                                                                                            1013
230
6
22
14
                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (0-048-116B-6 (1-306) x AAT04269 (1-1013)
                                                                                                                                                            Example 2; Page 65; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              2.31e-99
1151.00
86.8%
84.6%
                   ä
                   Marrack
                                                  WPI; 1995-320543/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      int Similarity:
   Local Similarity:
   Match:
                                                             P-PSDB; AAR82538
                                                                                                                                                                                                                                                                                                                                                                                                                 inment Scores:
                   Kappler JW,
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90
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gene alpha-2 domain"

beta-2 domain"

gene

domain"

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BP.
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/*tag= a
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P-PSDB; AAW29214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Major histocompatability complex fusion complex for modulating T celactivity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                              Edwards AC;
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Matches:
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                                                                                                                 95WO-US009816
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95US-00382454
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1145.00
87.2%
85.7%
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Chavaillaz P, Jiao J;
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P-PSDB; AAR98907.
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Local Similarity:
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                WO9604314-A1
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beta chains – useful for suppressing an immune response to an auto:immune
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                                                                                                                                                                                                                                             ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
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                  141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn
                                                                                             161 ValalaleSerLeuSerArgThrGluAlaLeuAsnHisHsisAsnThrLeuValCysSer
                                                                                                                                                           465 GFCGCCATCTCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG
                                                                                                                                                                                                                  ValThraspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGluGlu
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SCE1 single chain gene; ss.
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DNA; 1382

ACA60744;

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ACA60744 standard;
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disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, etc.
                                                                                               Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;
                                                               of major
                                                               the construction
                                                              The present sequence was used in the construction histocompatibility complex (MHC) fusion complexes
                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                       Example 17, Page 140-141; 217pp; English.
                                                                                                                                                                                              Gaps:
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1145.00
87.2$
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The invention relates to a major histocompatibility complex (WHC) fusion complex (I) comprising an WHC molecule that contains a peptide-binding groove, and a presenting peptide covalently (e.g. an antigenic peptide) [Inked to the MHC molecule, where (I) is capable of modulating the activity of a T cell. Also included are a DNA construct coding for the complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-As, or human HLA-DR1 (human leukocyte antigen-DR1), a wultivalent MHC to peptide that can modulate the activity of T cells (involving introducing that can modulate the activity of T cells (involving introducing control of the host cells under conditions sultable for expression of the Complex, and selecting host cells that express MHC fusion complex, and selecting host cells that axpress MHC fusion complex that modulate the activity of T cells), a single recombinant expression vector comprising DNA that codes for the alpha and beta chains of the fusion complex. Also included are inducing an immune competation of the fusion complex. Also included are inducing an immune complex, and sequence coding for a fusion complex. Also included are inducing an immune cresponse in a mammal including vaccinating a mammal including vaccinating a mammal including vaccinating a mammal and including vaccinating a mammal influence and dispersession of the fusion complex. Also included are inducing an immune cresponse in a mammal and including vaccinating a mammal including vaccinating a single chain fusion complex. On the mammal a DNA sequence comprising a fusion complex or not complex, or not complex, but a mammal and a mammal influence comprising a transmembrane domain, and a contain complex mind a contain a transmembrane domain, and a contain complex that is a real receptor (TCR) antagonist or partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis,
                                                                                                                                                                             MHC; major histocompatibility complex; gene therapy; fusion complex; peptide-binding groove; T cell modulation; class II MHC; vaccine; autorimmune disorder; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes mellitus; myasthenia gravis; immunogen; chronic allergy; mouse; ds; I-Ad; gene.
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                                                                                           Mouse MHC I-Ad/Ova 323-339 synthetic gene SCE1.
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95US-00382454.
97US-00776084.
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16-JUN-2003 (first entry)
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P-PSDB; ABU72108.
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01-FEB-1995;
17-JAN-1997;
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Synthetic.
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agonist and is covalently linked to the MHC protein, or DNA sequence coding for the fusion complex which is a single chain fusion molecule. The methods are useful for identifying a peptide that can modulate the activity of T calls, inducing an immune response in a mammal (including vaccinating a mammal against a targeted disorder) and for suppressing an immune response in a mammal. The disorders include an autoimmune disorder such as multiple sclerosis, insulin-dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or chronic allergies. The present sequence encodes a mouse MHC class II I-Ad fusion complex of the
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Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;

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                                                                                                                                                                                                                   SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
                                                                                                                                                                                                                                          GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg
                                                                                                                                                                                                                                                                                                                                                                                                                           GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyraspSeraspValGlyGluTyrargAlaValThrGluLeuGlyArgProAspAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValThrhspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greacagarrrcracccageccaagarcaaagrececreerrcaggaargeccaggagge
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                                                                                                                                                        MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu
                                                                                                                                                                                                                                                                                 41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly
                                                                                                                                                                                                                                                                                                                120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGGGGAAGC------GGCGGA
                                                                                                                                                                                                                                                                                                                                             G1yG1yG1yG1ySerG1uArgHisPheVa1Va1G1nPheLyeG1yG1uCysTyrTyrThrAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro
              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                          3-048-116B-6 (1-306) x ACA60744
              1.3e-98
1145.00
87.2
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ment Scores:
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--ACTAGTGGTGGCGGTGGCAGC 755
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/*teg= b
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/loce= "murine MHC class II I-Ad gene beta chain leader
gequence"
                                                                                                                                               MHC; major histocompatibility complex; PCR; polymerase chain reaction; T cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myasthenia gravis; ds.
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/*tbg= c
/labd= CVA 323-339
/note= "chicken ovalbumin residues 323-339"
138. .167
                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                //tag= d
/note= "10 residue linker peptide"
168. 452
                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "24 residue peptide linker"
107. .1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     class II I-Ad
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//label= I-Ad betal
//note= "murine MHC class II I-Ad
453. .734
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/label= I-Ad_alphal
/note= "murine MHC class
1068. .1352
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AGCCTGAAGAGCCCCCATCACTGTGGAGTGG-
                                                                                                                              Vector SSC1-derived single chain gene
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/label= I-Ad_alpha2
/note= "murine MHC c]
1353. .1382
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/label= I-Ad_beta2
/note= "murine MHC c
735. .806
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6. .1385
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                                                                         AAT17586 standard; DNA; 1385
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95US-00382454
                                                                                                             (first entry)
                   261 GlyGlyGlyGlySer
                                   Gecerrecreerrec
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01-FEB-1995;
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Chavaillaz P, Jiao J;

WPI; 1996-129343/13.
P-PSDB; AAR98905.

Major histocompatability complex fusion complex for modulating T cell activity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.

Example 17; Fig 27; 210pp; English.

AAT17586 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SSCI. The MHC fusion complex comprises at least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a transmembrane domain. DNA encoding a MHC fusion complex may be cloned into a host cell to express the complex. The transformed cells may then be used to identify peptides that modulate, pref. antagonise, T cell activity. DNA encoding a MHC fusion complex or a single chain fusion molecule may be used to vaccinate a mammal against a targeted disorder. The fusion complexes may be used to suppress an immune response in an animal suffering from an immune disorder e.g. multiple sclerosis, innul-dependent diabetes mellitus, rheumatorid arthritis, myasthenia gravis or chronic allergies. The complexes may also be used in the treatment of livestock and pets such as cate and dogs. The MHC fusion complexes can be produced such that they contain a single antigenic peptide including one. of known structure, additionally a wide range of peptides can be presented for T cell interaction
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Sequence 1385 BP; 316 A; 384 C; 398 G; 287 T; 0 U; 0 Other;

1385 227 24 10 3		alvalvalbeumetvalbeu 20 	erProSerLeuGluHisPro 40 :: CTGCTCACGCTGAA 119	euValProArgGlySerGly 60 GGCGGA 164	lyglucysTyrTyrThrasn 80 	BnArgGluGluTyrValarg 100 	euGlyArgProAspAlaGlu 120 	laGluValAspThrAlaCys 140 	rgargLeuGluGlnProAsn 160
Length: Matches: Conservative: Mismatches: Indels:	7586 (1-1385)	Metalaleuglnilebroserleuleuleuseralaalavalvalvalleumetvalleu 	SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro	IlevalvalSerGlySerTrpAspGlyGlyGlySerLeuValProArgGlySerGly	Glydlydlysergluarghiephevalvaldinpheryedlyglucysfyrfyrfhrasn 	Glythiglinargileargleuvalthrargfyillefyrabharggluglufyivalarg 	Tyraspseraspvalglyglutyrargalavalthrgluleuglyargfroaspalaglu 	Tyrtrpaenserginprogiuileleugiuargthrargalagiuvalaspthralacys 	ArghisabnTyrgluglyProgluThrSerThrSerLeuargargLeugluglnProabn
1.3e-98 1145.00 87.2% 70.7%	106) x AATI	leughnilePro	roglyThrgli caaggaccTT	'alSerGlySe' ::: !AAGCTGGTCG'	ilysergluar acrccgaaag	lnargilear paccaracc	SerAspValGl	NenSerGlnPr 	AsnTyrGluGl
<pre>jnment Scores: 1. No.: 5e: 2et Similarity: 1. Local Similarity 3y Match:</pre>	:0-048-116B-6 (1-306) x AAT17586	1 Metalal 6 ATGCTC	21 SerSerP 66 AGCAGCC	41 Ilevalv 20 ATCAACG	61 GlyGlyG 165 GGGGGAA	81 GlyThrG 225 GGGACGC	101 Tyrasps 285 TACGACA	121 TyrTrpA 345 TACTGGA	141 ArgHiBA 405 AGACACA

Alignment Scores:	Db 756 GGCGTGGTTCC 770
	WAT86987 standard; DNA; 1385 BP. WAT86987; WAT86987; T-MAR-1998 (first entry) SSC1 single chain gene. Construction; major histocompatibility complex; MHC; SSC1 single chain gene; 88. WAT86987; WHC; SSC1 single chain gene; 88. WHC; SSC1 single chain major histocompatibility complex comprise the chain major histocompatibility complex set a chain major histocompatibility complex set a chain major histocompatibility complex (MHC) fusion complexes the present sequence was used in the construction of sistocompatibility complex (MHC) fusion complexes the present sequence was used in the construction of sistocompatibility complex (MHC) fusion complexes
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XX SQ Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;	Wargebary standard; DNA; 1385 BP. Wargebary Wargebary
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ixample 17; Page 135-137; 217pp; English. The present sequence was used in the construction of instocompatibility complex (MHC) fusion complexes sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0	WAT86987 standard; DNA; 1385 BP. WAT86987; WAT86987; WAT86987; WAT86987; WAT86987; WAT81998 (first entry) WAT81999 (first entry) WAT8199 (first entry) WAT819 (first entry) WA
nellitus, ecc. Example 17; Page 135-137; 217pp; English. The present sequence was used in the construction of major istocompatibility complex (MHC) fusion complexes equence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other	WAT86987 standard; DNA; 1385 BP. WAT86987; WAT86987; WAT86987; WAT86987; WAT86987; WAT86987; WAT86987; WAT86987; WAT86987; WAT86988 (first entry) WAT86987; WAT86988 (first entry) WAT86988 (first entry) WAT86988 (first entry) WAT86000000000000000000000000000000000000
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ingle chain major histocompatibility complex comprising linked alpha beta chains - useful for suppressing an immune response to an auto:imm lisease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes hellitus, etc. Example 17; Page 135-137; 217pp; English. The present sequence was used in the construction of major istocompatibility complex (MHC) fusion complexes	AT86987 standard; DNA; 1385 BP. WAT86987; WAT86987; 77-MAR-1998 (first entry) SSC1 single chain gene. SO3 single chain gene; 88. Synthetic. Location/Qualifiers 61385 /*tag= a 109728191-A1. 17-AUG-1997. 10-JAN-1996; 96US-00596387. (DADE-) DADE INT INC. Thode PR, Jiao J, Burkhardt M, Wong HC;
PPI; 1997-402555/37. PPISDB; AAW29212. Single chain major histocompatibility complex comprising linked alpha seta chains - useful for suppressing an immune response to an auto:imm fleasae, e.g. multiple sclerosis, rheumatoid arthritis, diabetes callitus, etc. Example 17; Page 135-137; 217pp; English. The present sequence was used in the construction of major istocompatibility complex (MHC) fusion complexes sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;	11 187 187 187 187 187 187 187 187 187 1
thode PR, Jiao J, Burkhardt M, Wong HC; PPI; 1997-402555/37. PSDB; AAW29212. ingle chain major histocompatibility complex comprising linked alpha seta chains - useful for suppressing an immune response to an auto:lmm lisease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes hellitus, etc. Example 17; Page 135-137; 217pp; English. The present sequence was used in the construction of major histocompatibility complex (MHC) fusion complexes sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;	WAT86987 standard; DNA; 1385 BP. WAT86987; WAT86987; 77-MAR-1998 (first entry) SSC1 single chain gene. Construction; major histocompatibility complex; MHC; fusion complex ingle chain gene; ss. Synthetic. Wynthetic. Fey 6. 1385 Atag= a MO9728191-A1. MO-JAN-1997; 97WO-US001617.
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10-JAN-1997; 97WO-US001617. (DADE-) DADE INT INC. thode PR, Jiao J, Burkhardt M, Wong HC; PPI; 1997-402555/37. PPI; 1997-402555/37. PPISDB; AAW29212. Single chain major histocompatibility complex comprising linked alpha stata chains - useful for suppressing an immune response to an auto:imm teachains - useful for suppressing an immune response to an auto:imm stata chains - useful for suppressing an immune response to an auto:imm stata chains - useful for suppressing an immune response to an auto:imm stata chains - useful for suppressing an immune response to an auto:imm stata chains - useful for suppressing an immune response to an auto:imm stata chain major histocompatibility complex (MHC) fusion complexes the present sequence was used in the construction of major istocompatibility complex (MHC) fusion complexes sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;	11 187 187 187 187 187 187 187 186 187 187 187 187 187 187 187 187 187 187
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77-AUG-1997. 10-JAN-1997; 97WO-US001617. 11-JAN-1996; 96US-00596387. (DADE-) DADE INT INC. thode PR, Jiao J, Burkhardt M, Wong HC; PPI; 1997-402555/37. PSDB; AAW29212. Single chain major histocompatibility complex comprising linked alpha neta chain andor histocompatibility complex comprising linked alpha neta chain andor histocompatibility complex darthritis, diabetes neta chains - useful for suppressing an immune response to an auto: Immisease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes chailitus, etc. Example 17; Page 135-137; 217pp; English. The present sequence was used in the construction of major histocompatibility complex (MHC) fusion complexes Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;	NAT86987 standard; DNA; 1385 BP. NAT86987; NAT86987; 17-MAR-1998 (first entry) SSC1 single chain gene. SSC1 single chain gene; ss. Synthetic. Location/Qualifiers SSC3 single chain gene; ss. Incation/Qualifiers SSC3 single chain gene; ss.
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Location/Qualifiers 61385 /*tag= a 109728191-A1. 17-AUG-1997. 10-JAN-1997; 97WO-US001617. 11-JAN-1996; 96US-00596387. 11-JAN-1997; 97WO-US001617. 11-J	1187 AT86987 standard; DNA; 1385 BP. AT86987; AT86987; AT861998 (first entry) SC1 single chain gene. Construction; major histocompatibility complex; MHC; fusion complexisc1 single chain gene; 88.
inthetic. Location/Qualifiers 61385 61385 /*tag= a 109728191-A1. 17-AUG-1997. 10-JAN-1997; 97WO-US001617. 11-JAN-1997; 96US-00596387. 11-JAN-1996; 96US-00596387. 11-JAN-1996; 96US-00596387. 11-JAN-1996; 96US-00596387. 11-JAN-1996; 96US-00596387. 11-JAN-1997; 97WO-US001617. 11-JAN-1997; 97	r 11 187 VAT86987 standard; DNA; 1385 BP. VAT86987; 17-MAR-1998 (first entry) SSCI single chain gene.
Construction, major histocompatibility complex; MHC; fusion complex; iSC1 single chain gene; ss. Location/Qualifiers 61385 7*tag= a 109728191-A1. 17-AUG-1997. 11-JAN-1997; 97WO-US001617. 11-JAN-1996; 96US-00596387. 11-JAN-1997; 97WO-US001617. 11-JAN-1996; 96US-00596387. 11-JAN-1997; 97WO-US001617. 11-JAN	r 11 187 LAT86987 standard; DNA; 1385 B LAT86987; ?7-MAR-1998 (first entry)
SSCI single chain gene. Construction, major histocompatibility complex; MHC; fusion complex; SSCI single chain gene; ss. SSCI single chain gene; ss. Incation/Qualifiers 6. 1385 /*tag= a 109728191-A1. 17-AUG-1997; 197WO-US001617. 11-JAN-1996; 96US-00596387. 11-JAN-1997; 97WO-US001617. 11-JAN-1996; 96US-00596387. 11-JAN-1997; 97WO-US001617. 11-JAN-1996; 96US-00596387. 11-JAN-1997; 97WO-US001617. 11-JAN-1997; 97WO-US001617. 11-JAN-1997; 97WO-US001617. 11-JAN-1997; 97WO-US001617. 11-JAN-1996; 96US-00596387. 11-JAN-1997; 97WO-US001617. 11-JAN-1996; 96US-00596387. 11-JAN-1997; 97WO-US001617. 11-JAN-1997;	r 11 187 LAT86987 standard; DNA; 1385 B LAT86987;
17-MAR-1998 (first entry) 18C1 single chain gene. 18C1 single chain gene. 18C1 single chain gene. 18C1 single chain gene; 88. 18C1 single chain gene; 88. 18C2 single chain gene; 88. 18C3 single chain gene; 88. 18C4 single chain gene; 88. 18C5 single chain gene; 88. 18C6 single chain gene; 88. 18C7 single chain gene; 88. 18C8 single chain gene; 88. 18C8 single chain gene; 86. 18C9 single chain gene; 86. 18C9 single chain gene; 96. 1	r 11 887 AT96997 standard; DNA; 1385 B
WAT86987; 77-WAR-1998 (first entry) SCI single chain gene. Construction, major histocompatibility complex; WHC; fusion complex; SCI single chain gene: 88. SCI single chain gene; 88. SCI single chain gene; 88. SCI single chain gene; 88. SCI single chain major histocompatibility complex; WHC; fusion complex; SCI single chain gene; 88. SCI single chain gene; 86. SCI single	
756 ddcddrddrddrcc 770 5987 standard, DNA; 1385 BP. 6987 standard, DNA; 1385 BP. single chain gene. rruction; major histocompatibility complex; MHC; fusion complex; single chain gene; se. Location/Qualifiers 6. 1385 /*tag= a 28191-A1. 10-1997. AN-1996; 96US-00596387. E-) DADE INT INC. B- DADE INT INC. B- DADE INT SCOOMpatibility complex comprising linked alpha chains alor histocompatibility complex comprising linked alpha chains - useful for suppressing an immune response to an auto:imm ase, e.g. multiple solerosis, rheumatoid arthritis, diabetes ticus, etc. ple 17; Page 135-137; 217pp; English. present sequence was used in the construction of major occumpatibility complex (MHC) fusion complexes and 1385 BP; 316 A; 383 C; 339 G; 287 T; 0 U; 0 Other;	
261 GlyGlyGlyGlySer 265 756 GGCGTGTGGTGC 770 711 756 GGCGTGTGGTTCC 770 756 GGCGTGTGTGTCC 770 767 AT66987; 777-MAR-1998 (first entry) 78C1 single chain gene. 750 cation/Qualifiers 75. 1365 75. 1365 75. 1365 75. 1365 75. 1365 77. AUG-1997. 77. AUG-1997. 77. AUG-1997. 77. Aug-1996; 96US-00596387. 77. Aug-1996; 96US-00596387. 78DDE-) DADE INT INC. 78DDE-) DADE INT INC. 78DDE-) DADE INT INC. 78DDE-) Compatibility complex comprising linked alpha atec. a chain and or histocompatibility complex comprising linked alpha atec. a chain and or histocompatibility complex comprising linked alpha atec. a chain and or histocompatibility complex comprising linked alpha atec. a chain and or histocompatibility complex (MHC) fusion complexes 78 Manual 17, Page 135-137; 217pp; English. 78 DESERBER SEQUENCE WAS used in the construction of major instrocompatibility complexes 78 May 28 DESERBER SEQUENCE WAS USED ASSOCIATED ASSOCIATE	261 GlyGlyGlyGlySer
705 AGCCTGANGAGCCCATCATCGANGTGGACTAGTGGTGGCGCGCGCGCGCGCCCCCC 261 G1yG1yG1yG1ySer 265 756 GGCGTGGTGGTTCC 770 711 WT86587 standard, DNA; 1385 BP. WT86587; 77-MAR-1998 (first entry) SCI single chain gene; 88. STO 1385 BP. S	705 AdictighadadececcateatractighadadadActagragagagagagaga 75 261 GlyGlyGlyGlySer 265
241 Serically asserProllerhaval Glutrapargala GlusserGlusserAlabargserLys 705 Agcreadaga GcccContect Gadarga G	241 SerLeulysSerProileThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys
645 GTCHTCHTCHTCHTCHTCHTCHTCHTCHTCHTCHTCHTCHT	645 GTCATGCTGGATGATCCCTTCATCAGGGAGAGGTCTACACTGCCATGTGGAGCATCCC 241 SerLeulysSerProlleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys
221 ValMetLeuGluMerTh-ProHigh_IGI_VGIUVALTyrThrCyBlisValGlUHIPTOF 645 GTUTACTGAAAAACCCCTCATCGGGAAAAAAAAAAAAAAA	221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro [
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201 Thrivalchyalesree-Th-Gilliell [201 ThrValGlyValSerSerThrGlnLeuIleArgAanGlyAapTrpThrPheGlnValLeu
101 Third and third the condectable of the construction of major in the construction of major interesting in the construction of major interecompatibility complex complexes in the construction of major interesting interest	201 ThrvalGlyvalSerSerThrGlnLeu1leArgAsGCCCGGAATGGCCCAGGAGGAG 201 ThrvalGlyvalSerSerThrGlnLeu1leArgAsGGCTGGTTCAGGAATGGCCCAGGAGGAG 201 ThrvalGlyvalSerSerThrGlnLeu1leArgAsGGTTCTGTGTTCAGGGTCTTCCAGGTCTTGTGGGGGGTCTTGTAGGGATGGGGATGGGGGTCTTGTGGGGGTCTTGTGGGGGGTCTTGTGGGGGG
181 Valminappharytronlaivailatysinlar	181 ValThrAspPheTyrProAlaLysileLysValArgTrpPheArgAshanGlvGluGluGluGluGlid
465 GTGGCCGTGCTGCTGCTGCTGCTGCTGTGTGTGTGTGTTGT	465 Grödckircheckögackandagecerekaneeneereregreerregreerereregreerereregreereregreereregreereregreereregreereregreereregreereregreereregreereregreereregreereregreereregreereregreereregreeregreereregreereregreereregreereregreereregreereregreereregreereregreereregreereregreereregreereregreerereregreerereregreerereregreerereregreerererereregreerererereregreererererererererererereregreererererererererererererererererererer
161 ValAlalleSerleuSerArght-GludlaleuHenHighli] 465 GTGGCCARCTCCCCCTGCTGCAGAGAGGGCCCCCCAGACACACACACA	161 ValAlaileSerLeuSerArgThrGluAlaLeuAanHisHisAsnThrLeuValCysSer 161

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Mismatches:
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The invention relates to a major histocompatibility complex (MHC) fusion complex (I) comprising an MHC molecule that contains a peptide-binding groov, and a presenting peptide covalently (e.g. an antigenic peptide) crowplex (I) comprising an MHC molecule, where (I) is capable of modulating the cativity of a T call. Albo included are a DNA construct codaing for the complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-As, or human HLA-DRI (human leukocyee antign-DRI), a multivalent MHC fusion complex complex that modulate the activity of T cells (involving introducing peptide that can modulate the activity of T cells (involving introducing complex, that modulate the activity of T cells (involving introducing peptide that can modulate the activity of T cells (involving introducing culturing the host cells under conditions suitable for expression of the MHC fusion complex, and selecting host cells that express MHC fusion complex, that modulate the activity of T cells), a single recombinant expression vector complex that modulate the activity of T cells), a single recombinant complex that modulate the activity of T cells), a single recombinant complex that codes for T cell costimulatory factor and the alpha and beta chains of the MHC fusion complex. The DNA constructs can contain beta chains of the fusion complex. Also included are inducing an immune response in a mammal (including vaccinating a mammal against a targeted disorder, by administering on member response in a mammal (including vaccinating a mammal about suppression or member very modulation of the ministering and mamne response in a mammal and the conding for a fusion complex which is a single chain fusion complex of the member and is covalently linked to the MHC protein, or DNA sequence coding for the fusion complex which is a single chain fus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis,
WHC; major histocompatibility complex; gene therapy; fusion comple peptide-binding groove; T cell modulation; class II MHC; vaccine; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes mellitus; myasthenia gravis; immunogen; chronic allergy; mouse; ds; I-Ad; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grammer S,
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Chavaillaz P, Jiao JJJ;
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95US-00382454.
97US-00776084.
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01-FEB-1995;
17-JAN-1997;
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Sequence 1385 BP; 316 A; 383 C; 399 G; 287

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Location/Qualifiers
6. .1508
6. .439= a
6. .4409= b
/*tag= b
/label= I.Ad beta chain leader
sequentine MHC class II I-Ad gene beta chain leader
sequentine HRC class II I-Ad gene beta chain leader
                            MHC; major histocompatibility complex; PCR; polymerase chain reaction; T cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myasthenia gravis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Major histocompatability complex fusion complex for modulating T cell activity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.
       SCT1-derived single chain gene encoding MHC fusion complex
                                                                                                                                                                                                                                                                              /*tag= e
/label= I-Ad beta1
453. -734
/*tag= f
/label= I-Ad beta2
/label= "murine MHC class II I-Ad gene beta-2
/35. 806
                                                                                                                                                                                                  /*tag= c
/label= OVA 323-339
/note= "chicken ovalbumin residues 323-339"
138. 167
/*tag= d
/note= "10 residue linker peptide"
                                                                                                                                                                                                                                                                                                                                                                  / teage | 9

/ hotes | 24 residue peptide linker"

/ hotes | 1067

/ teage | 1-Ad_alphal

/ hotes | murine MHC class II I-Ad gene

1068. | 1352

/ tage | 1352

/ tage | 1 - Ad_alpha2

/ hotes | murine MHC class II I-Ad gene

1333. | 1505

/ tage | 1

/ hotes | murine MHC class II I-Ad gene

domain | hotes | murine MHC class II I-Ad gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grammer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 17; Fig 28; 210pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wong HC, Rhode PR, Weidanz JA,
Chavaillaz P, Jiao J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-00283302.
95US-00382454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-US009816
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P-PSDB; AAR98906.
                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-1994;
01-FEB-1995;
                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-FEB-1996
                                                                                                                                       sig_peptide
                                                                                   Synthetic
           Vector
                                                                                                       Key
140
                                                                                                                                                                                                                                                                                                                                                                                                              141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 ValAlaileSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValThrAspPheTyrProAlaLyslleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
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                                                                                                        20
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                                                                                                                                                 21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
                                                                                                       MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValLeuMetValLeu
                                                                                                                     6 ATGGCTCTGCAGATCCCCAGCCTCCTCTCAGCTGCTGTGGTGGTGGTGATGGTGCTG
                                                                                                                                                                                            41 IleValValSerGlySerTrpAspGlyGlyGlyGlyGlyGsrLeuValProArgGlySerGly
                                                                                                                                                                                                                  120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------GGCGGA
                                                                                                                                                                                                                                                                                                                                                                      TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys
                                                                                                                                                                                                                                                                                                                                                                                201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1385
227
4
24
10
3
         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                               Gaps:
                                                                                   (1-1385)
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                                                                                  10-048-116B-6 (1-306) x ACA60742
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          1.3e-98
1145.00
87.2%
85.7%
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                           cent Similarity:
: Local Similarity:
:y Match:
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  ument Scores
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465

121

181

705

241

756

AAT17587

261

alpha-transmembrane

gene

Edwards

domain

gene alpha-2

gene alpha-2

gene beta-1 domain"

AAT17587 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SCT1. The MHC fusion complex comprises at least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a transmembrane domain. DNA encoding a MHC fusion complex may be cloned into a host cell to express the complex. The transformed cells may then be used to identify peptides that modulate, pref. antagonise, T cell activity. DNA encoding a MHC fusion complex or a single chain fusion molecule may be used to vaccinate a mammal against a targeted disorder. The fusion complexes may be used to suppress an immune response in an animal suffering from an immune disorder e.g. multiple sclerosis, insulindependent diabetes mellitus, rheumacoid arthritis, myasthenia gravis or chronic allergies. The complexes may also be used in the treatment of livestock and pets such as casts and dogs. The MHC fusion complexes can be produced such that they contain a single antignic peptide including one of known structure, additionally a wide range of peptides can be presented for T cell interaction

Sequence 1508 BP; 337 A; 414 C; 440 G; 317 T; 0 U; 0 Other;

	1508	227	4	24	10	e
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	1.46e-98	1145.00	87.28	85.78	70.78	~
nment Scores:				Local Similarity:		

0-048-116B-6 (1-306) x AAT17587 (1-1508)

048-110	048-1108-0 (1-300 X MAII/30/ (1-1300/	
ч 9	MetalaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu 	20 65
21 66	SerSerProGlyThrGluGlyGlyAanSerIleCyaPheSerProSerLeuGluHiaPro	40
41	IlevalvalSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly	60 164
61	GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn 	80
81	GlyThrGlnArg1leArgLeuValThrArgTyr11eTyrAsnArgGluGluTyrValArg 	100
101	TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 	120 344
121	TyrTrpasnSerGlnBroGlu1leLeuGluargThrargalagluValaspThralaCys 	140
141	ArgHisasnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 	160 464
161	ValAlaileSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 	180 524
181	ValthraspphetyrProalatysileLysValargTrpPheArgAsnGlyGlnGluGlu 	200
201	ThrvalGlyvalSerSerThrGlnLeuileArgAsnGlyAspTrpThrPheGlnValLeu 	220

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Single chain major histocompatibility complex comprising linked alpha and beta chains - useful for suppressing an immune response to an auto:immune disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, etc.
                                     241 SerLeuLysSerProlleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
                                                Construction, major histocompatibility complex; MHC; fusion complex; SCT1 single chain gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence was used in the construction of major histocompatibility complex (MHC) fusion complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1508
227
4
24
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 17; Page 137-139; 217pp; English.
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                                                                                                                                                                                                                                                           Location/Qualifiers 6. .1508
                                                                                                                                                                                                                                                                                                                                                                                                    Rhode PR, Jiao J, Burkhardt M,
                                                                                                                                     AAT86988 standard; DNA; 1508 BP.
                                                                                                                                                                                                                                                                                                                                            97WO-US001617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.46e-98
1145.00
87.2%
85.7%
                                                                              261 GlyGlyGlySer 265
                                                                                                Geceracitatice 770
                                                                                                                                                                                                                                                                                                                                                              96US-00596387
                                                                                                                                                                            27-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                    /*tag= a
                                                                                                                                                                                               SCT1 single chain gene.
                                                                                                                                                                                                                                                                                                                                                                                 (DADE-) DADE INT INC.
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P-PSDB; AAW29213.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                               31-JAN-1996;
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                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                 Key
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97US-00960190

29-OCT-1997;

(SUNO-) SUNOL MOLECULAR CORP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerbeuLysSerProlleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
                                  165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224
                                                                                                                                                                                                                                                                                                     GlyThrGlnArglleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
                                                                                                                                                                                                                                                                                                                                                          284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValalaileSerLeuSerArgThrGlualaLeuAsnHisHisAsnThrLeuValCysSer 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Major histocompatibility complex; MHC; single chain MHC; sc-MHC; Ig; peptide binding groove; immunoglobulin; T cell receptor; immune response; immune-related disorder; antigenic peptide; fusion protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    645 greargeregagargaceereareaggaagagreracaeergeeargregagcareee 704
                                                                                                     9
SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro
                                                                                                                                                                                                                                                                                                                                                          225 GGGACGCAGGCCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                          405 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGGGGGGCTTGAACAGCCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 585 ACAGTGGGGGTCTCATCCACACACTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys
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                                                                                                                                                                                                     GlyGlyGlyGlyGluhrgHisPheValValGlnPheLysGlyGluCysTyrThrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 ileValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly
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                                                                                                                                                     120 Arcaacgaagcreerccrecracceaageceaaacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX89069 standard;
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The invention relates to new single chain major histocompatibility complex (sc-MHC) class II complexes that comprise a peptide binding groove, and a modified class II beta 2 chain or covalbantly linked care inwanced class II beta 2 chain or covalbantly linked cimmunoglobulin (Ig) light chain constant (CI) region. The MHC complexes are useful for detection and analysis of peptide ligands, pathogenic T-cells, for functional, cellular and molecular assays. They can be used to identify and isolate T cell receptor and/or MHC agonists and antagonists. They can also be used to cells involved in immune-related disorders. They can also be used to craise antibodies and to screen immune cells. It is also use in a method of suppressing an immune response in mammals. The sc-MHC complexes of suppressing an immune response in mammals. The sc-MHC complexes comprising midlied these form expressing cells in single antigent ceptides readily isolated from expressing cells in single antigent ceptides readily isolated from expressing cells in single complex. The polyspecific MHC complexes also provide a companion complex. The present sequence represents a DNA encoding a single chain complex. The present sequence represents a DNA encoding a single chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 TACGACAGCGACGTGGGCGAGTACCGCGGTGACCGGAGCTGGGGCGGCCAGACGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetalaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 Arcaacgaagcreergcragceaaceaaceaaceaaace------GGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly
                                                                                                                                                                           Single chain major histocompatibility complex class I complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;
                                                                                    HC;
                                                                                    Wong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                    Jiao
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                                                                                    Burkhardt M,
                                                                                                                                                                                                             Example 1; Fig 1; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.46e-98
1145.00
87.2%
: 85.7%
                                                                                      Acevedo J,
                                                                                                                      WPI; 1999-418411/35.
P-PSDB; AAY27111.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                      Rhode PR,
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98WO-US021520

13-OCT-1998,

sh completed: May 31, 2006, 23:17:04 :ime : 723 secs

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BC0326520 Mus muscu
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Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses
Patent: WO 0109194-A 1.08-FSB-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Original Bource text: Mus musculus (strain BALB/c, sub_species domesticus) spleen cDNA to mRNA.
The protein domains are as follows: first external protein domain The protein domains are as follows: first external protein domain (D1) at bases 93-356; second external protein domain (D2) at bases 639-791. [1] also sequenced the IA-alpha genes from mice of b,f,u and g haplotypes.

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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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Broolst.C.C., Mathis,D.J., Kanter,M.R., Williams,V.E. II and
McDevitt,H.O.
Regions of allelic hypervariability in the murine A alpha immune
                                                                                                                                                                                                                                                                                                                                                            TOTO 11:199449

antigen; cell surface glycoprotein; class II gene; glycoprotein; histocompatibility antigen; integral membrane protein; major histocompatibility complex.

Mus musculus (house mouse)

Mus musculus
A linear
haplotype)
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Mus musculus H-2 class II histocompatibility antigen, A-D alpha chain precursor, mRNA, complete cds.
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Mus.

1 (bases 1 to 771)

Go,M.; Wang,H. and Wang,Q.

Batablishment of pirRS- I-A(d) alpha beta and stable expression of

BALB/c mouse I-Ad alpha beta chain gene in NIH3T3 cell line
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Direct Submission
Submitted (29-OCT-2003) Lab of Transfusion Transfered virus,
Transfusion Institute Beijing, 27 TaiPing Road, Beijing 100039,
China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      699 TTTGAGCCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAAAACACAACTTGGGAATCTTG
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Unclassified.

JE (bases 1 to 4713)

RS Webb,S.R., Winqvist,O., Karlsson,L., Jackson,M.R. and Peterson,P.A.

MC class II antigen-presenting systems and methods for activating CD4+T cells

UAL Patent: US 6355479-A 7 12-MAR-2002;

Location/Qualifiers

J. 4713

ource /organism="unknown"
/mol_type="unassigned DNA"
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                                      24 ATGCCGTGCAGCAGCAGAGCTCTGATCTGGGGGTCCTCGCCCTGAACACCATGCTCAGCCTC 83
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Seguence 7 from patent US 6355479.
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/tissue_type="Mammary tumor. C3(1)"Tag model. Infiltrating
ductal carcinoma. 5 month old virgin mouse."
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                                                                                  SCO29620
Mus musculus histocompatibility 2, class II antigen A, alpha, mRNA
(cDNA clone MGC:25392 IMAGE:2609494), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: Jeffrey Green M.D.
Tisaue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: Baylor College of Medicine Human Genome
Sequencing Center.
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg.R.
Direct Submission
Submitsed (06-MAY-2002) National Institutes of Health, Mammalian
Submitted (06-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Etsflynrdhsffhksyllfipoddiydcynehwgleefylkhwebeipadbgstt
Tvychlglsvglygivgtipilgglrsggtsrhpgpl"
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Sciuropatchi; Murcidea; Muridae; Mus.

1 (bases 1 to 1110)

Straubberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Altschul, S.P., Zeeberg, B., Buetow, K.H., Schamen, C.M., Schuler, G.D.,

Altschul, S.P., Zeeberg, B., Buetow, K.H., Schamen, C.M., Hong, L.,

Ropkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, P.,

Biatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scapleton, M., Soares, W.M., B., Bonaldo, M.F., Casavant, T.L.,

Schetz, T.E., Browmstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abrameon, R.D., Mullahy, S.J., Boack, S.A., McEwan, P.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Botterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanailus, D.E.,

Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M.A.

Mammallan Gene Collection Program Team

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

AL Proc. Nat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC043925 1110 bp mRNA linear ROD 30-MAR-2005 Mus musculus histocompatibility 2, class II antigen A, alpha, mRNA (cDNA clone MGC:49437 IMAGE:4023996), complete cds.
                                 181 ileProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
                                                                                                                                                                                                                                                                                                                                                                  201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
                                                                                                                                                                                                                                                                                                                                                                                                            631 GTTCTGAAACACTGGGAACCTGAGATCCCCACCCCCATGTCAGAGGTGACAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
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BC043925.1 GI:27882597
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antigen: alpha domain"
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415. .630
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="MGI:95895"

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ThriysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                               Unclassified.

1 (bases 1 to 776)

Clark, B.R., Sharma, S.D. and Lerch, B.L.
MHC conjugates useful in ameliorating
Patent: US 6106840-A 4 22-AUG-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA"
                                                                                                                                                                                                                                                     776 bp
6106840.
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Sequence 4 from patent US
AR106256 AR106256.1 GI:12820786
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1078.00
94.18
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Best Local Similarity:
Query Match:
DB:
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Unknown.
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ACCESSION
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                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiML at: http://image.llnh.gov Series: IRAK Plate: 85 Row: f Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 31981715.
Location/Qualifiers
                                 be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214
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Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.
Young,A., Zhang,L.-H. and Green,E.D.
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                                                                                                                                                                                                                                          /note="gynonyme: Aalpha, IAalpha"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6"
                                                                                                             'organism="Mus musculus"
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                                                                                                                                                                                                                        1. .1110
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93.2%
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PAT 14-FEB-2001

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03-SEP-2003
                                    GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
                                                                                                                                                      PheGluProGlnGlyGlyLeuGlnAsn1leAlaAlaGluLysHisAsnLeuGly1leLeu 100
                                                                                                                                                                                                                                                                                                                                                        ameliorating autoimmunity
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Matches:
Conservative:
Mismatches:
Indels:
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Sharma, S.D., Lerch, L.B. and Clark, B.R.
MHC-mediated toxic conjugates useful in
Patent: US 194425-A 5 16-MAR-1993;
Anergen, Inc.; Redwood City, CA
                                                                                                                                                                                                                                                        AR363023
Sequence 5 from patent US 5194425.
AR363023
AR363023.1 GI:34423771
                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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1078.00
94.1%
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AR363023
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                                                                                                                                                                           ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
                                                        ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCCC
                    LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe
                              366 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTGTGGACAACATCTTC
                                                                                                                                                         546 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAACACTGGGGCCTGGAGGAGCCG
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1 (bases 1 to 776)

1 (bases 1 to 776)

1 (bases 1 to 776)

MHC conjugates useful in ameliorating autoimmunity Patent: US 6451314-A 4 17-SEP-2002;

Anergen, Inc.; Seattle, WA

1. coation/Qualifiers

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/organism="unknown""
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                                                                                                                                                                                                                                      DNA
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Sequence 4 from patent US 6451314.
AR229608.1 GI:27269264
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clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 40 Row: d Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13540710. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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/grain="mix FVB/N, C57BL/6J"
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/tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
/dl, gross tissue."
/clone_lib="NGL GAAP_MamS"
/lab_hōst="DH10B"
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/codon_start=1
/codon_start=1
/produce="histocompatibility 2, class II antigen A, alpha"
/prote=inid="kAH19721.1"
/db_xref="GEneID:14960"
/db_xref="GEneID:14960"
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ETSFFVNRDYSFHKLSYLTFIPSDDDIYDCKYEHWGLEEPVLKHWEPEIPAPMSELTF
TVVCALGLSVGLVGIVVGTIFIIQGLRSGGTSRHPGPL"
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 GlnSerProGlyAsp11eGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr
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/db_xref="GeneID:14960"
/db_xref="MGI:95895"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammallai; Butheria; Burchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Muridae; Mus.

Siraubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Rlausner, R.D., Colling, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheefer, T.B., Brownstein, M.J., Usdin, T.B., Toshlyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.B., McBwan, P.J., Morley, K.C., Hale, S., Garcia, A., Milan, J.W., Garcia, A., Maden, J.W., Gay, L.J., Lu, X., Gibbs, R.A., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.H., Sanilus, D.E., Schnerch, A., Schein, J. E., Jones, S.J. and Marra, M.A., Generatia, And Marra, M.A., And Marra, M.A., Generatia, And Marra, M.A., Ge
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                                                                                                         306 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGGGACTGTGTTCCCC 365
                                                                                                                                                                                                   LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
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Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 TTTGACCCCCAAGGTGGACTGCAAAACATAGCTGTAGTAAAACACAAACTTGGGAGTCTTG
                                                                                                                                                                                                                                                                                                                                                         Contact: MGC help desk
Email: cgapbe.r@mail.nl.gov
Tissue procurement: Lothar Hennighausen Ph.D., Robin Humphreys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC019721
BC019721.1 GI:18043825
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/clone="MGC:25391 IMAGE:3670758"
/tissue_type="Mammary tumor. WAP-TGP alpha model. 7 months
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 30 Row: c Coluum: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13540710.
Location/Qualifiers
Email: cgapbs-rômail.nih.gov
Tigabbs-rômail.nih.gov
Tigabbs-rômail.nih.gov
Tigabbs-rômail.nih.gov
Tigabbs-ròmail.nih.gov
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Tigabbs-ròmail.nih.gov
The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Contact: amg@bcm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTGGAGGTGAAGACGACATTGAGGCCGACCACGTAGGCACCTATGGTATAAGTGTATAT
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
/note=Vector: pCWV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.27e-103
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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KRausmer, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusins, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheefz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullah, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullah, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Shalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC031711 1100-000 mRNA linear ROD 30-JUN-2004 Mus musculus histocompatibility 2, class II antigen A, alpha, mRNA (cDNA clone MGC:25391 IMAGE:3670758), complete cds.
                                                                                             246 TITGACCCCCAAGGTGGACTGCAAAACATAGCTGTAGTAAAAACACAACTTGGGAGTCTTG 305
                                                                                                                                                                                                                                                             306 ACTAAGAGGTCAAATTCCACCCCAGCTACCAATGAGGCTCCTCAAGGGACTGTGTTCCCC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                      366 AAGTCCCCTGTGCTGCTGGGTCAGCCCAACACCCTCATCTGCTTTGTGGACAACATCTTC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluBro 200
                                                                                                                                                                                                                                                                                                                                                                                     121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 ProProValileAsnileThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 ATCCCTTCTGACGATGACATTTATGACTGCAAGGTGGAACACTGGGGCCTGGAGGAGCCG 605
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; EuteleosComi;
Mammalla; Butheria; Buarchoncoglires; Glires; Rodentia;
Sciurognathi; Muroides; Murinae; Mus.
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Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 ValLeuLygHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            606 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAGACT 662
                                            PheGluProGlnGlyGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu
                                                                                                                                                                                                                     ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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PUBMED
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AUTHORS
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DIGQYTFEFDGDELFYVDLDKKETVWMLPEFAQLRRFEPQGGLQNIATGKHNLEILTK
SKSTPATHARADATVPFKSPVLLGQDYTLICFVDNIPPVINITWLRNSKSYTDGVY
BTSFYVRDVSFHKLSYLTFIPSDDIYDCKVEHWGLBEPVLKHWEBEIPAPMSELTE
TVVCALGLSVGLVGIVVGTIFIIQGLRSGGTSRHPGPL
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gene (k haplotype), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluThrSerPheLeuValAsnArgAspHisSerPheHisBysLeuSerTyrLeuThrPhe 180
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M21931.1 GI:199493
cell surface glycoprotein; class II gene; integral membr protein; major histocompatibility complex.
Mus musculus
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/note="unnamed protein product; coding sequence"
/codon start=1 /codon start=1 /protein id="CAA24215.1"
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/db_xxef="CA:53077"
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Benoist, C.O., Mathis, D.J., Kanter, M.R., Williams, V.E. II and McDevitt, H.O.
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complementary DNA; histocompatibility antigen; signal peptide.
Mus musculus (house mouse)
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Proc. Natl. Acad. Sci. U.S.A. 80 (2), 534-538 (1983)
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Submitted (OS-MAY-1983)
Data kindly reviewed (OS-MAY-1983) k
Location/Qualifiers
1. 978
//db aref="Mus musculus"
//db xref="maxon:10090"
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'product="messenger RNA"
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Benoist, C.O.
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                                   181 IleproSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
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Matches:
Conservative:
Mismatches:
Indels:
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Sharma, S.D., Clark, B.R. and Lerch, B.L.
MHC class II-peptide conjugates useful
Patent: US 5468481-A 4 21-NOV-1995,
Amergen, Inc.; Redwood City, CA
Location/Qualifiers
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Sequence 4 from patent US 5468481.
AR365183
AR365183.1 GI:34428599
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/organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                                                                 Original source text: Mouse (strain BIO.H-2a4bp/Wts (2a4b)) spleen
B lymphocyte, cDNA to mRNA, clones alpha-[1,12].
B lymphocyte, cDNA to mRNA, clones alpha-[1,12].
Crafton, 18-JAM-1989.
Location/Qualiflers
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                                      . and Frelinger, J.A. not Ak, does not reflect
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/gene="MHC H2-I-A-alpha chain"
/gene="MHC H2-I-A-alpha chain mRNA"
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Matches:
Conservative:
Mismatches:
Indels:
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Bishop,G.A., McMillan,M.S., Haughton,G.
Signaling to a B-cell clone by Ek, but n
alteration of Ak genes
                                                                                                       Immunogenetics 28 (3), 184-192 (1988) 3137158
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                                                                                                                 | IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200
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                                                                                                                                                        366 AAGTCCCCTGTGCGGTGGGGTCAGCCCAACACCTCTGCTTTGTGGACAACATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 GlyGly-----GluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrThr
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Unclassified.

E 1 (bases 1 to 1508)

(S Rhode, P. R., Jaloo, J. -A., Burkhardt, M. and Wong, H.C. Single chain MHC complexes and uses thereof

AL Patent: US 5869270-A 122 09-FEB-1999;

Location/Qualifiers

1. .1508

/mol_type="unassigned DNA"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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AR031963.1 GI:5949568
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AR152030 Sequence
AR175030 Sequence
CS079300 Sequence
AX032544 Sequence
AX032544 Sequence
AX07354 Sequence
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BC01032 Mus muscu
M1548 Mouse MHC c
CQ777552 Sequence
M1548 Mouse MHC c
AX45202 Mus muscu
AX45222 Mus muscu
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Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses
Patent: WO 1019194-A 2 08-FEB-2001,
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
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/ Organism="synthetic construct"
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/db_xrefe"taxon:32630"

    .921
    /note="unnamed protein product"

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Seguence 2 from Patent WO0109194.
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Kappler, J. W. and Marrack, P.

Product and process for T cell regulation

Patent: US 5820866-A 25 13-OCT-1998;

Location/Qualifiers
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Kappler, J. W. and Marrack, P.

Product and process for T cell regulation
Patent: US 5820866-A 38 13-OCT-1998;

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1 (bases 1 to 4724)
Nebb,S.R., Winqvist,O., Karlsson,L., Jackson,M.R. and Peterson,P.A.
Webb,S.R., Winqvist,O., Karlsson,L., Jackson,M.R. and Peterson,P.A.
WHC class II antigen-presenting systems and methods for activating CD4+ T cells
Patent: US 6355479-A 8 12-MAR-2002;
Patent: US 6355479-A 8 12-MAR-2002;
1. cation/Qualifiers
1. .4724
/organism="unknown"
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Sequence 8 from patent US 6355479,
AR199666 GI:20249740
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                        SerSerProGlyThrGluGlyGlyAsnSerlleCysPheSerProSerLeuGluHisPro
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1 (bases 1 to 1382)
Rhode, P.R., Jao, J.-A., Burkhardt, M. and Collectules and uses thereof
Patent: US 6309645-A 123 30-OCT-2001;
        US-10-048-116B-6 (1-306) x AR033964 (1-1382)
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1 (bases 1 to 1382)
Rhode, P.R., Jiao, J.-A., Burkhardt, M. and Wong, H.C. Single chain MHC complexes and uses thereof Patent: US 5669270-A 123 09-FEB-1999;
Location/Qualifiers
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Mismatches:
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Mode, P.R., Jiao, J.A., Burkhardt, M. and MtC complexes and uses thereof Patent: BP 1526141-A 123 27-APR-2005;
Altor BioScience Corporation (US)
Location/Qualifiers
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Sequence 123 from Patent EP1526141.
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CS079301.1 GI:63093743

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PAT 29-SEP-1999
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TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGGCCGAGGTGGACACGGCGTGC
                                          6 ATGGCTCTGCAGATCCCCAGCTCCTCTCAGCTGCTGCTGTGGTGCTGTAATGCTG
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Rhode,P.R., Jiao,J.-A., Burkhardt,M. and Wong,H.C.
Single chain MHC complexes and uses thereof
Patent: US 5869270-A 121 09-FEB-1999;
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/organism="unknown"
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Weidanz, J.A. and wong, H.C.
Phrc complexes and uses thereof
Patent: EP 0991477-A 13 03-MAY-2000;
SUNOL MOLECULAR CORP (US)
                                          6 ATGGCTCTGCAGATCCCCCAGCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG
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    585 ACAGTGGGGGTCTCATCCACACACTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
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Sequence 123 from Patent EP0997477.
AX032545.
AX032545.1 GI:10279486
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PAT 06-MAY-2005
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                                                     66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA----- 119
                                                                                           TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
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            ATGGCTCTGCAGATCCCCAGCCTCCTCTCAGCTGCTGTGGTGGTGGTGTTGATGGTGCTG
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Patent: BP 1526141-A 121 27-APR-2005;
Altor BioSocience Corporation (US)
Location/Qualiflers
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1 (bases 1 to 1385)
3 Rhode, P.R., Jiso, J.-A., Burkhardt, M. and Wor MHC molecules and uses thereof
L. Patent: US 6309645-A 121 30-OCT-2001;
Location/Qualifiers
1. 1385
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Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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Mhc complexes and uses thereof
Parent: EP 0997477-A 121 03-MAY-2000;
SUNOL MOLECULAR CORP (US)
Location/Qualifiers
1385 bp I
121 from Patent EP0997477.

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Rhode, P.R., Acevedo, J., Burkhardt, M., Jiao, J.-a.
Soluble MHC complexes and methods of use thereof
Patent: US 622445-A 24 15-MAY-2001;
Location/Qualifiers
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3 1 (bases 1 to 1508)
S Rhode, P.R., Jiao, J.-A., Burkhardt, M. and Wong, J. Single chain MrC complexes and uses thereof
AL Patent: US 5865270-A 122 09 FEB-1999;
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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In (bases 1 to 1508)

S. Rhode, P.R., Jiao, J.-A., Burkhardt, M. and Wor

AL Patent: US 6309645-A 122 30-0CT-2001;

S. Location/Qualifiers

1. 1508

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Sequence 122 from patent US 6
AR175096.1 GI:17916395
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SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
                                                  GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn
                                                           ilevalvalSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly
                                                                            GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg
                                                                                                                                                                ThrValGlyValSerSerThrGlnLeulleArgAsnGlyAspTrpThrPheGlnValLeu
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OM protein

Run on:

Sequence:

Searched:

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Aav12068 Murine IA

Aat17588 Vector SC

Aat86989 SCE1 aing

Aca60744 Wouse MHC

Aat17586 Vector SS

Aat86987 SSC1 sing

Aca60742 Wouse MHC

Aat17587 Vector SS

Aat86988 SCT1 sing

Aca60743 Wouse MHC

Ad17598 Murine pc

Ad28609 Murine pc

Ad35099 Murine pc

Ab199038 Murine pc

Ab199038 Murine pc

Aag3170 Sequence

Aat3170 Sequence
                                                                                                                                                                                                            Ad56920 Mouse 1-A Ad56920 Mouse 1-A Ad56920 Mouse 1-A Ad59903 MBP 1-14 Ab199028 IAS MBP 1-14 Ab199020 IAS MBP 1-14 Ab199020 IAS MBP 1-14 Ab199020 IAS MBP 1-14 Ab199020 IAS MBP 9 Ab19903 MBP 90-10 Ad60705 CDNA enco Acc6700 CDNA enco Acc67150 Human maj Ad682150 Human maj Ad682150 Human maj Ad40822 DNA encod Ad724869 Breast ca Ad40822 DNA encod Ab63150 Rat seque Ad57995 Toxicity-Ab19775 Toxicity-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin; major histocompatibility complex; Fc region; antigen; T lymphocyte; immunostimulant; vaccine; infection; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding a fusion protein comprising a beta chain of MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                       ADJ75986
ADX26090
ABI99040
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AAQ03170
AAQ56920
AAQ56920
ABN84048
AAQ35055
AB199032
AB199021
AB199021
AB199021
AB199023
                                         AAT86989
ACA60744
AAT17586
AAT86987
ACA60742
AAT86988
AAX89069
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1. .921
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  AAF55099 standard; DNA; 921
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1049.5
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AAF55099
  -MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB spool/US10048116/runat_29062006_093309_10102/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US10048116/runat_29062006_093309_10102/app_query.fasta_1
-DB=N Geneseq_-QFWT=fastap_-SUPFIX=p2n.Trg -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosumed_0.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OOTPMT=pco -NORM=ext -HEAPSIXE=560 -MINLEN=0 -MXXLEN=2000000000 -HOST=abss05p
-OOTPMT=pco -NORM=ext -NORM=Ext -DSPHOORE -DOGOG_093309_10102 -NCPU=6 -ICPU=3
-NORMAP -NEG_SCORES=0 -WAIT -DSPHOORE -DOGOG_0BSV TIMEOUT=120
-NARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEOP=6 -FGAPEXT=7
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Aat04262 Hybrid IA
Adg31225 I-Ab(beta
                                                                    June 30, 2006, 01:23:04; Search time 522.277 Seconds (without alignments) 6007.369 Million cell updates/sec
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                                                                                                             US-10-048-116B-6_COPY_1_300
1572
1 MALQIPSLLLSAAVVVLMVL......KKKNAQLKWKLQALKKKLAQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
         GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                       5244920 segs, 3486124231 residues
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Maximum Match 100%
Listing first 45 summaries
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AAT04262
ADQ31225
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 200000000
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YGAPOP=10 Database :

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280 840

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GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCCTGCCATGTGGGAGCATCCC 720
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                   GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACACAAAAAACACTCTGGTCTGTTCG
                                                                  ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGluGlu
                                                                                        GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG
                                                                                                                                    ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu
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complement(158. .212)
/*tag= f //tag= #332 binding site"
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/note= "probable primer binding site (primer #270)"
511. .825
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/note= "probable primer binding site (primer #233)"
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>= "primer #333 (see AAT04263) binding site"
>389
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/note= "binding site for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= d
/note= "leader region"
complement(119. .172)
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                                                                                                                                                                                                                  The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histories) and complexible in which at least conscious that it is a dimer formed to its C-terminus, at least part of the Fc region of an immunoglobulin. The recombinant proteins, when linked to an antigenic peptide, are used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Ag-reactive T cells crown cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising a beta chain of MHC molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCCAAGGTGGACACGGCGTGC
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                                                                                                                    New soluble recombinant protein, useful e.g. as immunostimulant, comprises dimeric major histocompatibility complex molecule fused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 921 BP; 214 A; 265 C; 286 G; 156 T; 0 U; 0 Other;
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300
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                         Example 1; Page 34-35; 43pp; French.
(CNRS ) CNRS CENT NAT RECH SCI
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1572.00
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Best Local Similarity:
                                                                                  P-PSDB; AAB67481
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                                                                                                                                                                                                              TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACAAC
                                                                                                       GlyThrGlnArgileArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGACACAACTACGAGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT
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     GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrThrAsn
                                                                                                                                       GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC
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                                                                                                                                                                                                                                                                                                                                                                    TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGGCCGAGGTGGACACGGCGTGC
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/product= "I-Ab(beta)-Cholera toxin B subunit (CTB)-
leucine zipper (LZ)-BirA fusion cDNA"
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flow cytometry; mucous membrane invasive antigen;
I-Ab(beta)-cholera toxin B subunit-leucine zipper-BirA fusion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a hybrid IA beta chain gene, containing the chicken ovalbumin peptide (cOVA). This sequence was used in the construction of a hybrid IA alpha beta dimer. The encoded protein (pIAd-OVA) was found to be more stable than the IA alpha beta dimer. The stability was decreased by the addition of a MHC groove specific binding peptide (e.g. see AAR82527, AAR8258 and AAR82511), compared to an increase seen on the addition of a MHC binding peptide to IE k/dMCC. These complexes may be used to regulate an immune response. The complexes are capable of being recognised by a TCR alone or in combination with additional MHC proteins. These complexes are useful for therapeutic additional MHC proteins. These complexes are useful for therapeutic purposes and experimental purposes. They can also be used as reagents the treatment of diseases including autoimmune diseases, immunodeficiency diseases, immunoproliferation diseases, and graft-host rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.
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                                                                   /noce= "probable primer binding site (primer #271)"
532. .554
/*tag= k
hote= "probable primer binding site (primer #272)"
808. .836
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'note= "probable primer binding site (primer #232)"
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"IA beta chain beta 2 region"
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Matches:
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Mismatches:
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Best Local Similarity:
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                                                                                                                            601 GAGACGGIGGGGGICTCATCCACACACTGTTAGGAATGGGGACTGGACCTTCCAGGTC 660
                                                                                                                                                                    LeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHis 239
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/*tag= a
/product= "I-Ab (Deta) -Escherichia coli heat-labile toxin
B subunit (LTB)-leucine zipper (LZ)-BirA fusion protein"
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      SerValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGlu
                                            541 TCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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P-PSDB; ADQ31227.
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                                                           Peptide-Class II major histocompatibility complex (MHC) composite, useful for detecting antigen specific CD4+ T-cell, comprises antigen peptide containing epitope of mucous membrane invasive protein, and extracellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 GCGATCGCGGCCATCAGCATGGCGAACGGAGGTGGTCC---GGTGGAGGGGGGAAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 TGCAGACACACAATTACGAGGGCCGGAGACCCACACCTCCCTGCGGCGGCTTGAACAGCCC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 ProlleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 GlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 AsnGlyThrGlnArglleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 945 BP; 230 A; 256 C; 294 G; 165 T; 0 U; 0 Other;
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The invention relates to a novel class II major histocompatibility complex (MHC) antigenic peptide composite comprising a peptide containing the T-cell antigenic determinant of a mucous membrane invasive protein and the extracellular region of the class II MHC molecule or at least part of the extracellular region of the class II MHC molecule having an amino acid sequence comprising one or more deletions, substitutions or additions. The molecule of the invention may be useful for detecting an antigen-specific CD4+ T-cell by flow cytometry and for presenting a microorganism-derived mucous membrane invasive protein as an antigen. The method of the invention enables efficient detection of antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence is that of the class II major histocompatibility complex-related I-Ab (alpha)-Escherichia coli hear-labile toxin B subunit (ITB)-leucine
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Sequence 915 BP; 228 A; 242 C; 271 G; 174 T; 0 U; 0 Other;

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                                                                                                                                                                                              ProlleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySer
                                                                                                         MetAlaLeuGlnIlePro---SerLeuLeuLeuSerAlaAlaValValLeuMetVal
                                                                                                                       SerValThrAspPheTyrProAlaLyslleLysValArgTrpPheArgAsnGlyGlnGlu
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Matches:
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This nucleotide sequence comprises a PCR product obtained by amplification of mouse splenocyte cDNA using primers (see AAV12065 and AAV12066) designed for the amplification of Ind beta chain full-length cDNA. IAd alpha chain cDNA (see AAV12067) has been similarly obtained.

The IAd sequences were cloned into metallothionein promoter (see AAV12067)-driven vector pRMH=3 prior to sequencing. Major have compatibility complex (WHC) class II IAd heterodimers were expressed at the cell surface of transfected Drosophila Schneider 2 (ATCC CRL of 1974) cells. The invention relates to the preparation and use of synthetic antigen presenting matrices, in particular antigen presenting cells such as insect cells that have been transfected to produce MHC antigen presenting molecules with one or more accessory molecules. The matrices are used to activate naive CD4+ T cells and to shift the ongoing cutivation state into a preferred differentiated population of Th1 or Th2 cells. Applications include the treatment of autoimmune disease, e.g.
                                                                                                                                      804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Major histocompatibility class II antigen; MHC class II; T cell; T lymphocyte; Th1; Th2; activation; CD4+; antigen presenting cell; APC; autoimmune disease; diabetes; multiple sclerosis; autoimmune thyroiditis; systemic lupus erythromatosus; mysthemia gravis; Crohn's disease; inflammatory bowel disease; allergy; asthma; contact sensitivity; immunotherapy; therapy; IAd beta chain; mouse; ds; circular; cyclic.
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631 CTGGTCATGCTGGAGATGACCCCTCGGCGGGAGAGGTCTACACCTGTCACGTGGAGCAT 690
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                                                   CTGGTTCCGCGCGGATCCACTACAGCTCCATCAGCTCAGTTGAAAAGAAACTGCAGGCA
                                                                                                                                                                                                   CTTAAGAAAAGAACGCTCAGCTGAAGTGGAAACTTCAAGCCCTCAAGAAGAAACTGCCC
                                  ProSerLeuLysSerProlleThrValGluTrpArgAlaGlnSerGluSerAlaArgSer
                                                                                                        260 LysGlyGlyGlySerThrThrAlaProSerAlaGlnLeuLysLysLysLeuGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic antigen presenting cell for activating CD4+ T cells - use; treat autofimmune disease, e.g. diabetes, multiple sclerosis, Crohn's disease and inflammatory bowel disease, or allergy, e.g. asthma and contact sensitivity.
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diabetes, multiple sclerosis, autoimmune thyroiditis, systemic lupus erythematosus, myasthenia gravis, Crohn's disease and inflammatory bowel disease, or an allergy, e.g. asthma and contact sensitivity
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                                    4724 BP; 1196 A; 1194 C; 1200 G; 1134 T; 0 U; 0 Other;
                                                               4724 228
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Matches:
Conservative:
Mismatches:
Indels:
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(Bee AAT04270)"
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'note= "probable primer binding site (primer #270)"
31. .959
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/note= "probable primer binding site (primer #76)"
complement(40. .74)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               # 26) "
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note= "primer #365 (see AAT04272) binding site"
885. .403
                                                                    Major histocompatability complex; MHC; T-cell receptor; TCR; autolmune disease; immunodéficiency disease; immune response; immunoproliferation disease; graft-host rejection; therapy; B M12.C3; pM12-IAb-Ea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= m
/note= "probable primer binding site (primer
1000. .1013
/*tag= n
/note= "probable primer binding site (primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (primer
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product= "IA beta chain beta 2 region"
                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "leader region"
complement(140. .191)
/*tag= e
/note= "binding site for primer #363
complement(177. .226)
/*tag= f
                                                                                                                                                                                                                                                                                             /*tag= b
/note= "binding site for primer #362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "probable primer binding site 42. .976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "probable primer binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "probable primer binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "primer #364 binding site"
complement(212. .266)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/product= "hybrid IA beta chain"
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95WO-US002689
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                                  Hybrid IA beta chain gene
                                                                                                                                                                                                                                                                                                                                                                                                        b
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                                                                                                                                                                                                                                                                                                                                                                                   63. .143
/*tag= d
                                                                                                                                                                                                                                                                                                                                 63. .959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kappler JW, Marrack P;
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235 764

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Location/Qualifiers
6. 1382
6. 486
6. 86
7. 429 b
7. 429 b
7. 420 c
7. 420 b
7. 420 beta chain leader
7. 6. 86
7. 80 beta chain leader
7. 80 beta chain leader
                                                                                                                                                                                                                                                                                                                                                                                   MHC; major histocompatibility complex; PCR; polymerase chain reaction; I cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myasthenia gravis; ds.
                                                                                                         HisValGluHisProSerLeuLysSerProlleThrValGluTrpArgAlaGlnSerGlu
                                                                                                                             CACGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGGAGGGCACAGTCTGAG
                                                                 ThrPheGlnValLeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= I-Ad_alphal
/note= "murine MHC class II I-Ad gene alpha-2 domain"
1068. .1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "murine MHC class II I-Ad gene alpha-2 domain"
1353. .1379
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                                                                                                                                                                                                                                                                                                                                                         Vector SCE1-derived single chain gene encoding MHC fusion complex.
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/label= I-Ad_betal
/note= "muxine MHC class II I-Ad gene beta-1
453. .734
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138. 167
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/note= "10 residue linker peptide"
168. .452
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note= "24 residue peptide linker"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/label= OVA 323-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= I-Ad_alpha2
                                                                                                                                                                                                                                                               AAT17588 standard; DNA; 1382 BP.
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                                                                                                                                     셤
                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                             This sequence represents a hybrid IA beta chain gene. This sequence contains a fragment of the IE alpha chain (residues 56-73), as well as a linker and cleavage site. This sequence was transfected into a B cell line (M12.C3) using plasmid pM12-IAb-Ea. It was found that the encoded sequence was expressed in these cells. Complexes such as this may be used to regulate an immune response. The complexes are capable of being recognised by a TCR alone or in combination with additional MHC proteins. These complexes are useful for therapeutic purposes and experimental purposes. They can also be used as reagents for the treatment of diseases including autoimmune diseases, immunodeficiency diseases, immunoproliferation diseases, and graft-host rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCAGCCCAGGGACTGAGGGCGGAGACTCC----GAAGCTAGCTTTGAGGCTCAG 173
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                         Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.
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                                                                                                                                                                                                                                                                                                        Sequence 1013 BP; 220 A; 272 C; 327 G; 192 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                     1013
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                         Example 2; Page 65; 94pp; English.
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1151.00
86.8%
84.6%
73.2%
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Best Local Similarity:
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                                                                                                                                                                                                        524
                                                                                                                                                                                                                                                                                                                                                                        585 ACAGIGGGGGTCTCATCCACACCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644
                                                                                                                                                                                                                                                                                                                                                                                                                 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
                                                                                                                                                                                                                                                                                                                                                                                                                                             645 GTCATGCTGGAGATGACCCCTCATCAGGGAGGTCTACACCTGCCATGTGGAGCATCCC 704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys
                       345 TACTGGAACAGCCGGAGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGCGTGC
                                                                               ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn
                                                                                                         AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGGGGGGCTTGAACAGCCCAAT
                                                                                                                                                                                           465 GTGGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG
                                                                                                                                                                                                                                               ValThraspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGluGluGlu
                                                                                                                                                                                                                                                                                        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         major histocompatibility complex; MHC; fusion complex;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 GlyGlyGlyGlySer 265
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SCE1 single chain gene, ss.
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                                                                                                                                                                                                                                                                                                                                                                                 AAT17588 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SCEI. The MHC fusion complex comprises at least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a transmembrane domain. DNA encoding a MHC fusion complex may be cloned transmembrane domain. DNA encoding a MHC fusion complex may be cloned transmembrane complex that modulate, pref. antagonise, T cell activity. DNA encoding a MHC fusion complex or a single chain fusion complexes may be used to vaccinate a mammal against a targeted disorder. The fusion complexes may be used to suppress an immune response in an immal suffering from an immune disorder e.g. multiple sclerosis, insulince animal suffering from an immune disorder e.g. multiple sclerosis, insulince chronic allergies. The complexes may also be used in the treatment of livestock and pets such as cats and dogs. The MHC fusion complexes can be produced such that they contain a single antigenic peptide including one of known structure, additionally a wide range of peptides can be presented for T cell interaction
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                                                                                                                                                                                                                                                                Major histocompatability complex fusion complex for modulating T cel activity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.
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                                                                                                                                            Edwards AC;
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r P, Jiao J;
95WO-US009816
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95US-00382454
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Chavaillaz P,
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31-JUL-1995;
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                                                        Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;
             of major
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        The present sequence was used in the histocompatibility complex (MHC) fusi
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The invention relates to a major histocompatibility complex (MHC) fusion complex (I) comprising an MHC molecule that contains a peptide-binding growd, and a presenting peptide covalently (e.g. an antigenic peptide) linked to the MHC molecule, where (I) is capable of modulating the complex, where the MHC molecule is a class II MHC (e.g. mouse I.Ad or I.C. complex, where the MHC molecule is a class II MHC (e.g. mouse I.Ad or I.C. day, or human HLA-DR1 (human leukocyte antigen-DR1), a multivalent MHC fusion complex comprising two or more linked complexes, identifying a peptide that can modulate the activity of T cells (involving introducing introducing introducing the host cells cloning vectors that each contain the fusion complex DNA, culturing the host cells under conditions suitable for expression of the MHC fusion complex that modulate the activity of T cells), a single recombinant expression complex that modulate the activity of T cells), a single recombinant complex that modulate the activity of T cells), a single recombinant complex that modulate the activity of T cells), a single recombinant complex that codes for a T cell costimulatory factor and the alpha and beta chains of the MHC fusion complex. The DNA constructs can contain complex and beta chains of the MHC fusion complex. The DNA constructs can contain complex and beta chains of the fusion complex. Also included are inducing an immune response in a mammal directing DNA sequence comprising a fusion complex, or DNA sequence coding for a fusion complex which is a single chain fusion molecule that contains a transmembrane domain, and a presenting peptide that contains a transmembrane domain, and a presenting peptide that contains a single chain fusion molecule coding for the fusion complex which is a single chain fusion molecule coding for the fusion complex which is a single chain fusion molecule coding for the fusion complex which is a single chain fusion molecule coding for the fusion complex is a single chain fusion molecule coding for identificati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis,
                                                                                                                                                                         fusion complex;
                                                                                                                                                                  MHC; major histocompatibility complex; gene therapy; fusion compley peptide-binding groove; T cell modulation; class II MHC; vaccine; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes mellitus; myasthenia gravis; immunogen; chronic allergy; mouse; ds; I-Ad; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edwards AC;
                                                                                                                              Mouse MHC I-Ad/Ova 323-339 synthetic gene SCE1.
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95US-00382454.
97US-00776084.
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17-JAN-1997;
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MHC; major histocompatibility complex; PCR; polymerase chain reaction; T cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myasthenia gravis; ds.
                                                                                                                     Vector SSC1-derived single chain gene encoding MHC fusion complex
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1068. .1352
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label= I-Ad_alpha2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e PR, Weidanz JA,
Jiao J;
                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= j
/note= "6xHis
                                                     DNA; 1385
         756 GGCGGTGGTGGTTCC 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00283302
95US-00382454
                                                                                                                                                                                                                                                                                                 sequence"
87. .137
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DADE-) DADE INT INC
                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wong HC, Rhoc
Chavaillaz P,
                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                      feature
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                                                                                                26-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1994;
01-FEB-1995;
                                                                                                                                                                                                                                                       sig_peptide
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                                                                                                                                                                                                 Synthetic
                                                                         AAT17586;
                                                   AAT17586
                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                      misc
                            RESULT 10
                                                                                                                                                                                                                       Key
                                                            vaccinating a mammal against a targeted disorder) and for suppressing an immune response in a mammal. The disorders include an autoimmune disorder such as multiple sclerosis, insulin-dependent disbetes mallitus, rheumatoid arthritis, myasthenia gravis or chronic allergies. The present sequence encodes a mouse MHC class II I-Ad fusion complex of the
                                                                                                                                                                                                                                                                                                                                                                                                    100
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                                                                                                                                                                                                                                                                             120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGGGAAGC------GGCGGA
                                                                                                                                                                                                                                                                                                                                                     GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrThrAsn
                                                                                                                                                                                                                                                                                                                                                                         GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGGGAGTGCTACTACACCAAC
                                                                                                                                                                                                                                                                                                                                                                                                GlyThrGlnArg1leArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValAlaileSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerLeuLysSerProlleThrValGluTrpArgAlaGluSerGluSerAlaArgSerLys
                                                                                                                                                                                                                                                                                                         ilevalvalSerGlySerTrpAspGlyGlyGlyGiySerLeuValProArgGlySerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro
                                                                                                                                                                                                                   MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                        GGGACGCAGCGCATACGCCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGGCCATCTCCCTGTCCAGGACGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGACAGATTTCTACCCAGCCAAGATCCAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG
                                                                                   U; 0 Other
                                                                                                                                                                                            US-10-048-116B-6_COPY_1_300 (1-300) x ACA60744 (1-1382)
                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                 405 G; 284 T; 0
                                                                                                                                                                       Gaps:
                                                                               BP; 320 A; 373 C;
                                                                                                                 8.31e-101
1145.00
87.2%
85.7%
72.8%
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                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                Sequence 1382
                                                                                                     Ignment Scores
                                                           invention
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DB:
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Location/Qualifiers
6. .1385
7*tag= a
6. .86
1.86
1.4.bg= b
1.1.bp= 1-Ad beta chain leader
7.00te= "murine MHC class II I-Ad gene beta chain leader
                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "murine MHC class II I-Ad gene alpha-2 domain"
353. .1382
                                                                                                                                                                                                                                                                                                                                                                                  domain
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note= "24 residue peptide linker"
07. .1067
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note≕ "10 residue linker peptide'
[68. ,452
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/label= OVA_323-339
/note= "chicken ovalbumin
138. .167
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                                                                                                                                                                                                           /*tag= e
/label= I-Ad_beta1
/note= "murine MHC class
453. .734
                                                                                                                                                                                                                                                                          label= I-Ad_beta2
note= "murine MHC class
335. .806
                                                                                                                                                                                                                                                                                                                                                                                class
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P-PSDB; AAR98905.
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ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
                                                                                                                                                          645 GTCATGCTGGAGATGACCCCTCATCAGGGAGGGTCTACACCTGCCATGTGGAGCATCCC 704
                                                                                                                                                                                                         SerLeuLysSerProlleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
                                                                                                                                                                                                                             Single chain major histocompatibility complex comprising linked alpha and beta chains - useful for suppressing an immune response to an auto:immune disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, etc.
                                                                                          585 ACAGTGGGGGTCTCATCCACACACACTTATAGGAATGGGGACTGGACCTTCCAGGTCCTG
                       525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG
ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGluGlu
                                                                   ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Construction; major histocompatibility complex; MHC; fusion complex; SSC1 single chain gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1385 BP, 316 A, 383 C, 399 G; 287 T, 0 U, 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence was used in the construction of major histocompatibility complex (MHC) fusion complexes
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227
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 17; Page 135-137; 217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
6..1385
/*tag≈ a
                                                                                                                                                                                                                                                                                                                                                                                      BP.
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1145.00
87.2%
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72.8%
                                                                                                                                                                                                                                                                              261 GlyGlyGlyGlyser 265
                                                                                                                                                                                                                                                                                                GCCGCTGCTTCC 770
                                                                                                                                                                                                                                                                                                                                                                                    AAT86987 standard; DNA; 1385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSC1 single chain gene
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P-PSDB; AAW29212.
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Percent Similarity;
Best Local Similarity:
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Pred. No.:
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181
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                                                                                                         AAT17586 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SSC1. The MHC fusion complex comprises at least one MHC molecule containing a poptide-linding groove and a presenting peptide covalently linked to the MHC molecule and opt. a transmembrane domain. DNA encoding a MHC fusion complex may be cloned into a host cell to express the complex. The transformed cells may then ce used to identify peptides that medulate, pref. antagonise, T cell may then complex or a single chain fusion molecule may be used to vaccinate a mammal against a targeted disorder. The fusion complexes may be used to suppress an immune response in an animal suffering from an immune disorder e.g. multiple sclerosis, insulince chaonic allergies. The complexes may also be used in the treatment of livestock and pets such as cats and dogs. The MHC fusion complexes can be produced such that they contain a single antigenic peptide including one of known structure, additionally a wide range of peptides can be presented for T cell interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 AGCAGCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA---- 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn
         Major histocompatability complex fusion complex for modulating T cell activity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1385 BP; 316 A; 384 C; 398 G; 287 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1385
227
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                              Example 17; Fig 27; 210pp; English.
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1145.00
87.2%
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Pred. No.:
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chronic allergy; mouse; ds; I-Ad; gene.

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ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGluGlu 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
                                                                                                                                                                                                                              GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACTGGAACAGCCAGCCGGAGATCTTGAACGCGGGCCCAAGGTGGACACGCGGCGTGC 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGTGGGGGTCTCATCCACACACCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyThrGlnArglleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 TACGACAGCGACGTGGGCGAGTACCGCGGTGACCGAGCTGGGGCGGCCCAGACGCCGAG 344
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                                                                                                                                                                                                                                                                                                                                                                           120 ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGCGGAAGC--------GGCGGA 164
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                                                                                                                                                                                    21 SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
                                                                                                                                                                                                                                                                                                             41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly 60
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                                                              1 MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu
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US-10-048-116B-6_COPY_1_300 (1-300) x AAT86987 (1-1385)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACA60742 standard; DNA; 1385 BP.
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ID ACA6

XX AC ACA6

XX AC ACA6

XX BDT 16-J

XX MHC;

XW MHC;

XW AUC;

XW AUC;

XW INBU
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The invention relates to a major instruction to complex (I) comprising an MMC molecule that contains a peptide-binding complex (I) comprising an MMC molecule that contains a peptide-binding of groove, and a presenting peptide covalently (e.g. an antigenic peptide) inked to the MHC molecule, where (I) is capable of modulating to the complex, where the MHC molecule is a class II MHC (e.g. moulating for the complex, where the MHC molecule is a class II MHC (e.g. moulating for I. Also included are antigen-DRI), a multitualent MHC fusion complex comprising two or more linked complexes, identifying a peptide that can modulate the activity of T cells (involving introducing into host cells cloning vectors that each contain the fusion complex will be complex that modulate the activity of T cells (involving introducing into host cells under conditions suitable for expression of the MHC fusion complex will protein, a single recombinant expression vector comprising DNA that codes for the alpha and beta chains of the MHC fusion complex. The DNA constructs and complex will peptide sequences and Kozak sequence for efficient capable and beta chains of the MHC fusion complex. The DNA constructs and contain cherecologous leader peptide sequences and Kozak sequence for efficient capable and suppression of the fusion complex. Also included are inducing an immune response in a mammal (including vaccinating a mammal by administering DNA sequence comprising a transmembrand by administering complex winch is a single recent of the fusion complex which is a single forth of molecule that contains a transmembrand domain, and a cull length MHC molecule that contains a transmembrand domain, and a cull length MHC molecule that contains a transmembrand by administering peptide that contains a transmembrand and suppressing an immune response in a mammal grained a targeted disorder, and secure coding for the fusion complex which is a single chain a mammal disorder become coding for the fusion complex which is a single chain an expension of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to a major histocompatibility complex (MHC) fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           Edwards AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1385
227
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                         Rhode PR, Weidanz JA, Grammer S, P, Jiao JJJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 17; Fig 27; 126pp; English.
                                                                                                                                                                                                                    94US-00283302.
95US-00382454.
97US-00776084.
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1145.00
87.2%
                                                                                                                                                                              06-JUL-2001; 2001US-00900379
                                                                                                                                                                                                                                                                                                     (DADE-) DADE INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ABU72106.
                                                                                               US2002198144-A1
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                                                                                                                                                                                                                                                                                                                                                                  Chavaillaz P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1385
                                                                                                                                                                                                                    29-JUL-1994;
01-FEB-1995;
17-JAN-1997;
                                                                                                                                       26-DEC-2002
                                        Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allergies.
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                                                                                                                                                                                                                                                                                                                                             Nong HC,
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/*tag= j
/label= I-Ad_alpha-TM
/noce= "murine MHC class II I-Ad gene alpha-transmembrane
domain"
                                                                                                       /*tag= b
/label= I-Ad_beta_chain_leader
/note= "murine MHC class II I-Ad gene beta chain leader
sequence"
87. .137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT17587 encodes a murine MHC fusion complex capable of modulating T cactivity encoded by the vector SCT1. The MHC fusion complex comprises least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a
                                                                                                                                                                                                                                                                                                                                                                             II I-Ad gene alpha-2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                       domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Major histocompatability complex fusion complex for modulating T celactivity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.
    T cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myasthenia gravis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                       II I-Ad gene alpha-2
                                                                                                                                                                                                                                                             beta-1
                                                                                                                                                                                                                                                                                                       beta-2
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                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                              /*tag= c
/label= OVA 323-339
/note= "chicken ovalbumin residues
138. 167
                                                                                                                                                                                                       /*tag= d
/note= "10 residue linker peptide"
168. .452
                                                                                                                                                                                                                                                                                                                           *tag= g
note= "24 residue peptide linker"
107. .1067
                                                                                                                                                                                                                                                            II I-Ad
                                                                                                                                                                                                                                                                                                    'note= "murine MHC class II I-Ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grammer S,
                                                                                                                                                                                                                                                                                                                                                       /*tag= h
/label= I-Ad_alphal
/note= "murine MHC class
1068. .1352
                                                                                                                                                                                                                                                          /note= "murine MHC class
                                                                                                                                                                                                                                                                                                                                                                                                                       class
                                                              Location/Qualifiers 6. 1508 /*tag= a 6. .86
                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= i
/label= I-Ad_alpha2
/note= "murine MHC o
                                                                                                                                                                                                                                                 /label= I-Ad betal
                                                                                                                                                                                                                                                                                  '*tag= f
'label= I-Ad beta2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weidanz JA,
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95US-00382454
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Chavaillaz P, Jiao J;
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                                                                                                                                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9604314-A1
                                                                                                sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-FEB-1996
                                              Synthetic.
                                                                  Key
    AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA----- 119
                                                                                                                                                                  224
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                                                                                                                                                                                       GlyGlyGlySerGluArgHisPheValValGlnPhelysGlyGluCysTyrThrAsn
|||||||
|GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC
                                                                                ATGGCTCTGCAGATCCCCAGCCTCCTCCTCTCAGCTGCTGTGGTGCTGATGGTGCTG
                                                            MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValLeuMetValLeu
                                                                                                                                               41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly
                                                                                                                                                                                                                                 GlyThrGlnArgileArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg
                                                                                                                                                                                                                                             TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu
                                                                                                                                                                                                                                                                                        141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn
                                                                                                                                                                                                                                                                                                                                                                            405 AGACACAACTACGAGGGCCGGAGACCAGCACCTCCCTGCGGGGGGGTTGAACAGCCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                      ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                     ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHC; major histocompatibility complex; PCR; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                     TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCT1-derived single chain gene encoding MHC fusion complex.
   24
10
                                        US-10-048-116B-6_COPY_1_300 (1-300) x ACA60742 (1-1385)
 Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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 85.78
72.8%
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-1996
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transmembrane domain. DNA encoding a MHC fusion complex may be cloned into a host cell to express the complex. The transformed cells may then be used to identify peptides that modulate, pref. antegonise, T cell activity. DNA encoding a MHC fusion complex or a single chain fusion molecule may be used to vaccinate a mammal against a targeted disorder. The fusion complexes may be used to suppress an immune response in an animal suffering from an immune disorder e.g. multiple sclerosis, insulindependent diabetes mellitus, rheumacoid arthritis, myssthenia gravis or chronic allergies. The complexes may also be used in the treatment of livestock and pets such as cats and dogs. The MHC fusion complexes can be produced such that they contain a single antigenic peptide including one of known structure, additionally a wide range of peptides can be presented for T cell interaction
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Single chain major histocompatibility complex comprising linked alpha and beta chains - useful for suppressing an immune response to an auto:Immune disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes
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The invention relates to new single chain major histocompatibility complex (sc-MHC) class II complexes that comprise a peptide binding groove, and a modified class II beta 2 chain or covalently linked camplex, and a modified class II beta 2 chain or covalently linked immunoglobulin (Ig) light châin constant (I) region. The MHC complexes are useful for detection and analysis of peptide ligands, pathogenic T-cells, for functional, cellular and molecular assays. They can be used to cidentify and isolate T cell receptor and/or MHC agonists and antagonists. They can also be used to calls involved in immune-related disorders. They can also be used to craise antibodies and to screen immune cells. It is also use in a method of suppressing an immune response in mammals. The sc-MHC complexes of suppressing an immune calls in the sc-MHC complexes comprising modified class II beta 2 chains and/or Ig-c1 regions are comprising modified class II beta 2 chains and/or Ig-c1 regions are soluble and provide enhanced yield. These MHC complexes also can contain significant quantities. The polyspecific MHC complexes also provide a means to detect cells expressing multiple target structures with a single complex. The present sequence represents a DNA encoding a single chain
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|||| ATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGGGGGGAAGC--------GGCGGA
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                                                                                                         Single chain major histocompatibility complex class I complexes
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Best Local Similarity:
Query Match:
DB:
                                                                     P-PSDB; AAY27111
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Search completed: June 30, 2006, 01:48:14 Job time : 528.277 secs

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BC010322 Mus muscu
M13537 Mouse MHC c
CQ777552 Sequence
AF015280 Mus muscu
AR106257 Sequence
AR229609 Sequence
AR363024 Sequence
AR3648 Mouse MHC c
BC008168 Mus muscu
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Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses
Patent: WO 01919194-A 2 08-FEB-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGCTCTGCAGATCCCCAGCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG
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Best Local Similarity 100.0%; Pred. No. 4.8e-256;
Matches 918; Conservative 0; Mismatches 0;
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AR229609
AR363024
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VERSION
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Listing first 45 summaries
                                                                                                - nucleic search, using sw model
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                                                                             / Match 75.8%; Score 696.2; DB 2; Local Similarity 94.6%; Pred. No. 2.6e-191; nes 748; Conservative 0; Mismatches 28;
      1 (bases 1 to 893)
Kappler, J. W. and Marrack, P.
Product and process for T cell regulation
Patent: US 5820866-A 25 13-OCT-1998;
Location/Qualifiers
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RESULT 4 AR033964 LOCUS DEFINITION Sequence 123 from patent US 5869270. ACCESSION AR033964.1 GI:S949569 VERSION AR033964.1 GI:S949569 TITUE ORGANISM UNKNOWN. UNCLASSION AR033964.1 GI:S949569 SOURCE ORGANISM UNKNOWN. UNCLASSICION AR033964.1 GI:S949569 SOURCE ANTHORS SINGLE PR. N. Jaco, J. A., Burkhardt, M. and Wong, H.C. TITUE JOURNAL PATHORS ANTHORS		Query Match 66.2%; Score 607.8; DB 2; Length 1382; Best Local Similarity 89.6%; Pred. No. 1.7e-165; Matches 673; Conservative 0; Mismatches 57; Indels 21; Gaps 1;	ATGGCTCTGCAGATCCCCAGCCTCCTCTCAGCTGCTGGGTGGTGGTGCTG 60	9y 61 AGCAGCCCGGGACTGAGGCGGAAACTCCATCTGGCGTGGCTGGAGCACCCG 120	Oy 121 ATCGTGGTGTCCGGCAGCTGGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180 Db 105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGGGG	Qy 181 GGTGGAGGTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGCGAGTGCTACTACACCAAC 240 Db 165 GGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGCGAGTGCTACTACACCAAC 224	Qy 241 GGGACGCAGCATACGCCTCGTGACCAGATACATCTACAACCGGAGGAGGAGTACGTGCGC 300 Db 225 GGGACGCAGCGCATACGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 284	Qy 301 TACGACAGACGAGGGGGGGGGGGGGGGGGGGGGGGGGGG	Qy 361 TACTGGAACAGCCGGAGATCCTGGAGCGAACACGCGGCCGAGCTGGACACGGCGTGC 420 Db 345 TACTGGAACAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACGCGGCCCAAGGTGGACGCGGGCCGAGGTGC 404	Qy 421 AGACACAAACTACGAGGGCGGGAGCCCCAGCGCGGGGGGGCTTGAACAGCCCAAT 480 Db 405 AGACAAACTACGAGGGCCGGAGACCACCCCTGCGGGGGGCGCTTGAACAGCCCAAT 464	Qy 481 GTCGCCATCTCCCTGTCCAGGACAGGCCCTCAACCACACACTCTGGTCTGTTCG 540	Qy 541 GTGACAGATTTCTACCCAGGCCAAGATGAGCTGGTTCAGGAATGGCCAGGAGGAG 600 [Qy 601 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGACTTGGACCTTCCAGGTCCTG 660 Db 585 ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 644	Qy 661 GTCATGGGGAATGACCCCTCATCAGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 720
AR047957 Sequence 38 from pater AR047957 AR047957.1 GI:5970300 Unknown. Unknown. Unclassified. I (bases 1 to 1013) I (bases 1 to 1013) Rappler, J. W. and Marze Product and process for Patent: US 5820866-A in 1013 Location/Qual //mol_type="un"	Query Match 69.5%; Score 637.6; DB 2; Length 1013; Best Local Similarity 89.5%; Pred. No. 3.3e-174; Matches 698; Conservative 0; Mismatches 79; Indels 3; Gaps 1;	OY 1 ATGGCTCTGCAGATCCCCAGCCTCCTCTCAGCTGCTGGTGGTGGTGGTGGTGGTG 60	Oy 61 AGCAGCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTGGAGCACCGG 120	OY 121 ATCGTGTCTCCGGCAGCTGGGAGGTGGGGGCTCACTAGTGCCCCCAGGCTCTGGA 180	OY 181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGCGGGTGCTACTACACCAAC 240	QY 241 GGGACGCAGCATACGGCTCGTGACCAGTACATCTACAACCGGGAGGAGTACGTGCGC 300	Qy 301 TACGACAGGACAGGCGAGTACCGCGCGGTGACCGAGCCGGCCAGACCGACC	Qy 361 TACTGGAACAGCCGAGATCTGGAACGCAGAGCGGCCCAAGTGAACACGCGTGC 420 Db 420 TACTGGAACAGCCGGAGATCCTGGAGCGAGCCGAGGTGGACGCGGAGCTGGACGTGGAACGCGGAGGTGGAACGCTGGAACGCGAGCTGGAACGCTGGAACGCTGGAACGCTGGAACGCTGGAACGCTGGAACGCTGGAACGCTGGAACGCTGTGC 479	Qy 421 AGACACAACTACGAGGGCCGGAGACCACACCTCCCTGCGGCGCGCTTGAACAGCCCAAT 480	QY 481 GTCGCCATCTCCCTGTCCAGACAGAGGCCCTCAACCACACACA	QY 541 GTGACAGATTTCTACCGAGGCGAAGATGAGGCGCTGGTTGAGGAATGGCCAGGAGGAG 600	Qy 601 ACAGTGGGGGTCTCATCCACACCTTATTAGGAATGGGGACTCGACCTTCCAGGTCCTG 660	Qy 661 GTCATGCTGGAGATCTGATCAGGAGAGATCTACACCTGCCATGTGGAGCATCCC 720 Db 720 GTCATGCTGGAGATGACCCCTCGGCGGGAGAGGTCTACACCTGTCACGTGGAGCATCCC 779	Oy 721 AGCCTGAAGAGCCCCATCACTGGAGGGGGCACAGTCGGAGCTGGCGGGAGCAAG 780

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0; Mismatches 57;
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QY 541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGG 600 Db 525 GTGACAGATTTCTACCCAGCCAGGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGG 584 QY 601 ACAGTGGGGGTCTCATCCACAGCTTATTAGGAATGGCCACTGGACCTTCCAGGTCCTG 660 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 7 AX032545 LOCUS LOCUS BERNITION Sequence 123 from Patent EP0997477. AX032545 AX032546 AX032545 AX032545 AX032546 AX032545 AX032545 AX032546 AX032545 AX032545 AX032546 AX032545 AX032546 AX032545 AX032546 AX032545 AX032546	66.2%; Score 607.8; DB 2; Length 1382; similarity 89.6%; Pred. No. 1.7e-165; Conservative 0; Mismatches 57; Indels 21; Gaps	1 ATGGCTCTGCAGATCCCCAGCCTCCTCTCAGCTGCTGGTGGTGCTGATGGTGTG 60	61 AGCAGCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120	121 ATCGTGGTGTCCGGCAGCTGGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA 180	181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGCCGAGTGCTACTACACCAAC 240 	241 GGGACGCAGCGCATACGGCTCCTGACCAGATACATCTACCACCGGGAGGAGTACGTGCGC 300	301 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG 360 	361 TACTGGAACAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC 420 	421 AGACACAACTACGAGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT 480

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MHC complexes and uses thereof
Patent: Bp 1526141-A 121 27-APR-2005;
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   AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGGGGTTGAACAGCCCAAT
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                                                                                                  GTGGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACACTCTGGTCTGTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown.
Unclassified.
1 (bases 1 to 1385)
1 (bases 1 to 1385)
1 MHC molecules and uses thereof
Patent: US 6309645-A 121 30-OCT-2001;
Location/Qualifiers
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                                                                                                                                                                                                                                                                            AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
                                                                                                                                                                                                                                                                                                                                                            Sequence 121 from patent US 6309645. ARI75095

    1385
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                      105 GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGGAGGGGGCGGAAGCGGCGGA
                                                            GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCCAAC
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1 (bases 1 to 1508)
Rhode, P.R., Jiao, J.-A., Burkhardt, M. and Wong, H.C. Single chain MHC complexes and uses thereof Patent: US 5819270-A 122 09-FEB-1999;
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89.6%; Pred. No. 1.8e-165;
ative 0; Mismatches 57;
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Sequence 122 from patent
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Mer complexes and uses thereof
Patent: EP 0991477-A 121 03-MAY-2000;
SUNOL MOLECULAR CORP (US)
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                                                   TACGA CAGCGA CGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACCCCGAG
                                                               TACTGGAACAGCCAGCGGCGGAGATCCTGGAGCGAACGCGGGCCGAGCTGGACACGGCGTGC
                                                                                                                  TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGGCGTGC
                                                                                                                                               AGACACACTACGAGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT
                                                                                                                                                                       AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGCGCTTGAACAGCCCAAT
                                                                                                                                                                                             GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG
                                                                                                                                                                                                                                                          585 ACAGTGGGGGTCTCATCCACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
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Sequence 121 from Patent EP0997477.

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	181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGGTTCAAGGGCGAGTGCTACACCAAC 165 GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 241 GGGACGCATACGGCTCGTGACCAGATACATCTACAACCGGAAGGAGTACGTGCGC 241 GGGACGCAGAGCATACGTGACCAGAAACATCTACAACCGGAAGGAGTACGTGCGCC 241 GGGACGCAGACATACGTGACATACATCTACAACCGGGAGGAGTACGTGCGCCCAGAAACATACAACCGGGAAGGAGTACGTGCGCCCAGAAAACAACCGGGAAGGAGTACGTGCGCCAGAAAACAACCGGCAAGAACAACAACAACAACAAC	301 TACGACAGCACGTGGGGAGTACCGCGGGTGACCAGGCGGGGCGGCGAGAGGCGAGGGGGGGG		Qy 481 GTCGCCATCTCCTGTCCAGACAGAGCCCTCAACACCACAACATCTGGTCTGTTCG 540	Qy 541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600	Qy 601 ACAGTGGGGTCTCATCACACACACTTATTAGGAACTGGACTTCCAGGTCCTG 660	GTCATGCTGGAGATGACCCCTCATCAGGGAGA 	Oy 721 AGCCTGAAGACCCCATTCACTGGAGTGGA 751	/mol_type="unassigned DNA"
Qy 61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120 Db 66 AGCAGCCCAAGGAC 1 1 1 1 1 1 1 1 1 1	241 GGGACGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGGACGCGCGCG	1 1 1 1 1 1 1 1 1 1	Oy 481 GTCGCCATCTCCCTGTCAGACGCCCTCAACCACCACACACTCTGGTTCG 540	Oy 541 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 600	Oy 601 ACAGTGGGGGTCTCATCCACACAGTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 660	Oy 661 GTCATGCTGGAGATGACCCCTCATCAGGGAGGGTCTACACCTGCCATGTGGAGCATCCC 720	Oy 721 AGCCTGAAGACCCCATCACTGTGGAGTGGA 751 Db 705 AGCCTGAAGAGCCCATCACTGGGAGTGGA 735	E 8	Similarity 89.6%; Pred. No. 1.8e-165; 3; Conservative 0; Mismatches 57; Indels 21

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Length 1508, Indels 164

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61 AGCAGCCCCGGGACTGAGGCCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
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                                                           Score 607.8; DB 2;
Pred. No. 1.8e-165;
0; Mismatches 57;
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 Score 607.8; DB 2;
Pred. No. 1.8e-165;
0; Mismatches 57;
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MHC complexes and uses thereof
Patent: Ep 1556141.A 122 27-APR-2005;
Altor BioScience Corporation (US)
Location/Qualifiers
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Sequence 122 from Patent EP1526141.
CS079300. GI:63093742
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Perfect score:

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Sequence:

Scoring table:

Searched:

Database

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New soluble recombinant protein, useful e.g. as immunostimulant, comprises dimeric major histocompatibility complex molecule fused to immunoglobulin Fc region.
                                                                                                                                                                                                                                                                                                                                                                                             Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin; major histocompatibility complex; Pc region; antigen; T lymphocyte; immunostimulant; vaccine; infection; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                             DNA encoding a fusion protein comprising a beta chain of MHC.
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                           AAQ56920
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ABI99038
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                 WPI; 2001-182944/18.
P-PSDB; AAB67481.
WO200109194-A1
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Listing first 45 summaries
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Result No.

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The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the Fc region of an immunoglobulin. The recombinant proteins, when linked to an antigenied, pare used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or count and determents, and (to purify and/or enrich Ag-reactive T cells from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising a beta chain of MHC molecules
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/note= "binding site for primer #331 (see AAT04261)"
complement(158. .212)
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note= "binding site for primer #261 (see AAT04260)"
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/note= "probable primer binding site (primer #272)"
308. .836
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/note= "probable primer binding site (primer #233)"
complement(45. .74)
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note= "probable primer binding site (primer #259)"
377. .893
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/note= "probable primer binding site (primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= 9
note= "primer #333 (see AAT04263) binding
371. .389
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/note= "primer #332 binding site"
complement(199, .250)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "hybrid IA beta chain"
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/note= "leader region"
complement(119. .172)
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1. .16
/*tag= a
                                                                                                                                                                                 CATCATCATCATCAT 918
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/product= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide-Class II major histocompatibility complex (MHC) composite, useful for detectring antigen specific CD4+ T-cell, comprises antigen peptide containing epitope of mucous membrane invasive protein, and extracellular region of MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I-Ab(beta)-Cholera toxin B subunit-leucine zipper (LZ)-BirA fusion cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    class II major histocompatibility complex; MHC; CD4+ T-cell detection; flow cytometry; mucous membrane invasive antigen; I-Ab(beta)-cholera toxin B subunit-leucine zipper-BirA fusion; CTB; ss;
   GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG
                                                                                                                                           ACAGTGGGGGTCTCATCCACACGTTATTAGGAATGGGGACTGGACTTCCAGGTCCTG
                                                      GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGAG
                                                                                                                                                                                    GTCATGCTGGAGATGACCCCTCATCAGGGAGGTCTACACCTGCCATGTGGAGCATCCC
                                                                                                                                                                                                                   706 Greandergandaccerearcadadadacteracacerergeangaacareee
                                                                                                                                                                                                                                                    AGCCTGAAGAGCCCCCATCACTGTGGAGGGAGAGCACAGTCCGAGTCTGCCCGGAGCAAG
                                                                                                                                                                                                                                                                                      766 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "I-Ab(beta)-Cholera toxin B subunit (CTB)-
leucine zipper (LZ)-BirA fusion cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SENT-) SENTAN KAGAKU GLJUTSU INCUBATION CENT KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 10; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-2002; 2002JP-00351818
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P-PSDB; ADQ31224.
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Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a hybrid IA beta chain gene, containing the chicken ovalbumin peptide (COVA). This sequence was used in the construction of a hybrid IA alpha beta dimer. The encoded protein (plAd-OVA) was found to be more stable than the IA alpha beta dimer. The stability was decreased by the addition of a MHC groove specific binding peptide (e.g. see AAR82527, AAR82528 and AAR82511), compared to an increase seen on the addition of a MHC binding peptide to IE k/d-MCC. These complexes may be used to regulate an immune response. The complexes are capable of being recognised by a TCR alone or in combination with additional MHC proteins. These complexes are useful for therapeutic purposes and experimental purposes. They can also be used as reagents for the treatment of diseases including autoimmune diseases, immunodeficiency diseases, immunodeficiency
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                                                                                                                                                                                                                             Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 893 BP; 204 A; 239 C; 275 G; 175 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 75.8%; Score 696.2; DB 2; Il Similarity 94.6%; Pred. No. 1.9e-151; 748; Conservative 0; Mismatches 28;
                                                                                                               (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY
                                                                                                                                                                                                                                                                                                Example 1; Page 53; 94pp; English
                                                95WO-US002689
                                                                                94US-00207481
                                                                                                                                                Marrack P;
                                                                                                                                                                               WPI; 1995-320543/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                03-MAR-1995;
                                                                                04-MAR-1994;
                  08-SEP-1995
                                                                                                                                                Kappler JW,
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acid sequence comprising one or more deletions, substitutions or additions. The molecule of the invention may be useful for detecting an antigen-specific CD4+ T-cell by flow cytometry and for presenting an microorganism-derived mucous membrane invasive protein as an antigen. The method of the invention enables efficient detection of antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence is that of the class II major histocompatibility complex-related I-Ab(alpha)-Cholera toxin B subunit (CTB)-leucine zipper (LZ)-BirA fusion
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                                                                                                                                                                                                                             GTGGTGCTGATGGTGCTGAGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCG
                                                                                                                                                                                                                                                                                   CCGTCGCTGGAGCACCCGATCGTGGTGTCCGGCAGCTGGGACGTGGGGGGCTCACTA
                                                                                                                                                                                                                                                                                                                                         GTGCCCCGAGGCTCTGGAGGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGC
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                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                 9
                                                                                                                                                                     Length 945;
                                                                                                                                           Sequence 945 BP; 230 A; 256 C; 294 G; 165 T; 0 U; 0 Other;
                                                                                                                                                                                               0, Mismatches 108; Indels
                                                                                                                                                                     DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       883 AAGAAGAAACTCGCCCAGCATCATCATCATCAT 918
                                                                                                                                                                    Score 665.2; DB ]
Pred. No. 3e-144;
                                                                                                                                                                  72.5%;
                                                                                                                                                                    Query Match 72.5
Best Local Similarity 86.6
Matches 759; Conservative
                                                                                                               CDNA of the invention.
                                                                                                                                                                                                                             43
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for primer #362 (see AAT04270)"
                                                                                                                                                                                                                                                                                                                                    primer #363 (see AAT04271)"
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note= "probable primer binding site (primer #272)"
123. .850
                                                                                                                             Major histocompatability complex; MHC; T-cell receptor; TCR; autoimmune disease; immunodeficiency disease; immune response; immunoproliferation disease; graft-host rejection; therapy; B cell; M12.C3; pM12-IAb-Ea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= j
note= "probable primer binding site (primer #271)"
44. .568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (primer #259)"
                                                                                                                                                                                                                                                                                                                                                                                                                      #270) #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #366) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= n
/note= "probable primer binding site (primer #59)"
                                                                                                                                                                                                                 /*tag= a
/note= "probable primer binding site (primer #76)"
complement(40. .74)
                                                                                                                                                                                                                                                                                                                                                                                           site"
                                                                                                                                                                                                                                                                                                                                                                                  /*tag= g
/note= "primer #365 (see AAT04272) binding si
885. .403
/*tag= h
/note= "probable primer binding site (primer 331. .959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "IA beta chain beta 2 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gite
          915
                                                                                                                                                                                                                                                                                                                                                        /*tag= f
/note= "primer #364 binding site"
complement(212, .266)
                                                                                                                                                                                                                                                                               "hybrid IA beta chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= m
note= "probable primer binding
.000. .1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer binding
/*tag= e
/note= "binding site for
complement(177. .226)
                                                                                                                                                                                                                                                                                         63. .143
/*tag= d
/note= "leader region"
complement(140. .191)
                                                                                                                                                                                                                                            /*tag= b
/note= "binding site
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     % /*tag= 1
/*note= "probable p
942. .976
                                                        BP.
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                                                        DNA; 1013
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                                                                                                                                                                                                                                                                      /*tag= c
/product= '
                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= i
/product=
                                                                                             (first entry)
                                                                                                             Hybrid IA beta chain gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                          535. .564
                                                                                                                                                                                                                                                             63. .959
                                                                                                                                                                                                        . .18
*tag≃
                                                        standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAR-1995;
                                                                                            16-APR-1996
                                                                                                                                                                                                                                                                                                                  primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer_bind
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                                                                                                                                                                                                                                                                                         sig_peptide
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                                                                                                                                                                             Synthetic
          880
                                                        AAT04269
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                                             RESULT
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660 ACGGTGGGGCTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 719
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                      ADQ31228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss; gene.
                                                            661
                                                                                                                                                                                                                                                                                RESULT 5
AD031228
ID AD031228
XX AD04
XX AD04
XX C1as
XX C1as
XX I-low
XX I
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                                                                                                                                                                                                                                                                                                                       This sequence represents a hybrid IA beta chain gene. This sequence contains a fragment of the IE alpha chain (residues 56-73), as well as a linker and cleavage site. This sequence was transfected into a B cell line (M12.C3) using plasmid pM12-IAb-Ba. It was found that the encoded sequence was expressed in these cells. Complexes such as this may be used to regulate an immune response. The complexes are capable of being recognised by a TCR alone or in combination with additional MFC proteins. These complexes are useful for therapeutic purposes and experimental purposes. They can also be used as reasgents for the treatment of diseases including autoimmune diseases, immunodefliciency diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
                                                                                                                                                                       Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGCTCTGCAGATCCCCAGCCTCCTCTCAGCTGCTGTGGTGGTGGTGATGGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ATCGTGGTGTCCGGCAGCTGGGACGAGGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCAACATTGCTGTCGACAAGGCTGGAGGTGGTC---CGGTGGAGGGGGAAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACGACAGCGACGTGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCGAGGTGGACACGCGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1013 BP; 220 A; 272 C; 327 G; 192 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoproliferation diseases, and graft-host rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81;
  IMMUNOLOGY & RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 634; DB 2; I
Pred. No. 5.1e-137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 69.1%; Score 634; DB Best Local Similarity 89.1%; Pred. No. 5.1e Matches 695; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                           Example 2; Page 65; 94pp; English
JEWISH CENT
                                                 Marrack P;
                                                                                                   WPI; 1995-320543/41.
P-PSDB; AAR82538.
NAT
                                               Kappler JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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The invention relates to a novel class II major histocompatibility complex (MHC) antigenic peptide composite comprising a peptide containing the T-cell antigenic determinant of a mucous membrane invasive protein and the extracellular region of a class II MHC molecule or at least part of the extracellular region of the class II MHC molecule having an amino acid sequence comprising one or more deletions, substitutions or additions. The molecule of the invention may be useful for detecting an antigen-specific CD4+ T-cell by flow cytometry and for presenting a microorganism-derived mucous membrane invasive protein as an antigen. The method of the invention enables efficient detection of antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence is that of the class II major histocompatibility complex-related I-Ab(alpha)-Escherichia coli heat-labile toxin B subunit (LTB)-leucine
                                                                                                                                780
                                                                                                                                                                         Peptide-Class II major histocompatibility complex (MHC) composite, useful for detecting antigen specific CD4+ T-cell, comprises antigen peptide containing epitope of mucous membrane invasive protein, and extracellular region of MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "I-Ab(beta)-Escherichia coli heat-labile toxin
B subunit (LTB)-leucine zipper (LZ)-BirA fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 flow cytometry; mucous membrane invasive antigen;
I-Ab(beta)-heat-labile toxin B subunit-leucine zipper-BirA fusion; LTB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        class II major histocompatibility complex; MHC; CD4+ T-cell detection;
720 GTCATGCTGGAGATGACCCCTCGGCGGGGAGAGTCTAYACCTGTCACGTGGAGATCCC
                                                                                                                           721 AGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCCGAGTCTGCCCGGAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I-Ab(beta)-E. coli heat-labile toxin B subunit-LZ-BirA fusion cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 915;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zipper (LZ)-BirA fusion cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 628.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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Single chain major histocompatibility complex comprising linked alpha and beta chains - useful for suppressing an immune response to an auto: immune disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, etc.
                                                                                                                                                                                                                                                                                                                                                          AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCCG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACTGGAACAGCCGGACATCCTCGAGCGAACGCGGGCCGAGGTGGACACGGGGTGC
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                                                                                                                                                                                                                                                                                                                      ATGGCTCTGCAGATCCCCAGCCTCCTCTCAGCTGCTGTGGTGGTGCTGATGGTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC
                                                                                                                                                                                                                                                                                Length 1382;
                                                                                                                                                                                                                                                           Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;
                                                                                                                                                                                                                                   of major
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                                                                                                                                                                                                                                 The present sequence was used in the construction histocompatibility complex (MHC) fusion complexes
                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                                                 Score 607.8; DB 2;
Pred. No. 6.5e-131;
0; Mismatches 57;
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                                                                                                                Burkhardt
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89.6%;
                                                        97WO-US001617
                                                                           96US-00596387
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Best Local Similarity 89.6
Matches 673; Conservative
/*tag=
                                                                                              (DADE-) DADE INT INC
                                                                                                                                   WPI; 1997-402555/37.
                                                                                                                 PR, Jiao J,
                                                                                                                                             P-PSDB; AAW29214.
                                                                            31-JAN-1996;
                                                        30-JAN-1997;
                   WO9728191-A1
                                     07-AUG-1997
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                                                                                                                                                                                                                                    GTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAACG
                                         GAGGTGGTAGTGAAAGGCATTTCGTGTAACCAGTTCATGGGCGAGTGCTACTTCACCAACG
                                                                 GGACGCAGCGCATACGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGCT
                                                                             ACGACAGGGACGTGGGCGAGCACCGCGGGTGACCGAGCTGGGGGCGGCCAGACGCGAGT
                                                                                                                                              ACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCCGAGGTGGACACGGCGTGCA
                                                                                                                                                                                   GACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAATG
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                                                                                                                                                                                                                          | TOGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCGG
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                                                                                                                                                                                                                                                                                                                                            TCATGCTGGAGATGACCCCTCATCAGGGAGGTCTACACCTGCCATGTGGAGCATCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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           ;
 8.9e-136;
thes 54; Indels
 Pred. No. 8.96); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 6. .1382
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91.94;
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TGCATCATATTCTGGAT
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           677; Conservative
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Similarity
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104 180 164 240 224 300 284 360 344 420 404 480 464 540 524 600

65

Gaps

21;

beta chains of the MHC fusion complex.

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644
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 ACAGTGGGGGTCTCATCCACACACTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
                    ACAGTGGGGGTCTCATCCACACACACTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
                                                                  Greatscreakardaccecercareagadadareraceceraceargadadecaree
                                            GTCATGCTGGAGATGACCCCTCATCAGGAGGGTCTACACCTGCCATGTGGAGCATCCC
                                                                                                                                                                                                                                                           MHC; major histocompatibility complex; gene therapy; fusion complex; peptide-binding groove; T cell modulation; class II MHC; vaccine; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes mellitus; myasthenia gravis; immunogen; chronic allergy; mouse; ds; I-Ad; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weidanz JA, Grammer S, Edwards AC;
                                                                                                                                                                                                                                       Mouse MHC I-Ad/Ova 323-339 synthetic gene SCE1.
                                                                                                    AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
                                                                                         751
                                                                                       AGCCTGAAGAGCCCCATCACTGTGGAGTGGA
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95US-00382454.
97US-00776084.
                                                                                                                                                                    ACA60744 standard; DNA; 1382
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                                                                                                                                                                                                                 16-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jiao JJJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DADE-) DADE INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003-341126/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhode PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABU72108
                                                                                                                                                                                                                                                                                                                                                                US2002198144-A1.
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17-JAN-1997;
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Synthetic.
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heterologous leader peptide sequences and Kozak sequence for efficient expression of the fusion complex. Also included are inducing an immune response in a mammal against a targeted disorder, by administering bMA sequence comprising a fusion complex, or DNA sequence coding for a fusion complex which is a single chain fusion molecule) and suppressing an immune response in a mammal by administering to the mammal a DNA sequence comprising a transmembrane domain, and a full length MHC molecule that contains a transmembrane domain, and a presenting peptide that is a T cell receptor (TCR) antagonist or partial agonist and is covalently linked to the MHC protein, or DNA sequence coding for the fusion complex which is a single chain fusion molecule. The methods are useful for identifying a peptide that can modulate the activity of T cells, inducing an immune response in a mammal against a targeted disorder; and for suppressing an immune response in a mammal against a targeted disorder; and in sequence cuch as multiple sclerosis, insulin-dependent diabetes mellitus, then transment allowed as mouse MHC class II I-Ad fusion complex of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
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                                                                                                                                                                                                                                                                                                                                                                                                              DB 8;
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les 57;
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0; Mismatches
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Pred. No. 6.5
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11 Similarity 89.6%;
673; Conservative
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The invention relates to a major histocompatibility complex (MHC) fusion complex (I) comprising an MHC molecule that contains a peptide-binding groove, and a presenting peptide covalently (e.g. an antigenic peptide). Inked to the MHC molecule, where (I) is capable of modulating the complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-Ag, or human HLA-DRI (human leukocyte antigen-DRI)), a multivalent MHC tusion complex comprising two or more linked complexes, identifying a peptide that can modulate the activity of T cells (involving introducing into host cells cloning vectors that each contain the fusion ocmplex DNA, culturing the host cells under conditions suitable for expression of the MHC fusion complex, and selecting host cells that express MHC fusion complex, and selecting host cells that and beta chains complex that modulate the activity of T cells), a single recombinant expression vector comprising DNA that codes for the alpha and beta chains of the fusion complex MHC protein, a single recombinant expression vector comprising DNA that codes for a T cell costimulatory factor and the alpha

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           GGGACGCACGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGGCG
                                                  285 TACGACAGGACGTGGGGGAGTACCGCGGGGGGACCTGAGGCTGGGGCGGCCAGACGCGAG
                                                                                                                                                                           601 ACAGTGGGGGTCTCATCCACACACTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
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                                      AGACACAACTACGAGGCCGGAGACCAGCACCTCCCTGCGGCGCCTTGAACAGCCCAAT
                                                                                                                                   405 AGACACAACTACGAGGGCCGGAGACCAGCACCTCCCTGCGGGGGGTTGAACAGCCCAAT
                                                                                                                                                                GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG
                                                                                TACTEGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGGCCGAGGTGGACACGGCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHC; major histocompatibility complex; gene therapy; fusion complex; peptide-binding groove; T cell modulation; class II WHC; vaccine; autofimmune disorder; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes mallitus; myasthenia gravis; immunogen; chronic allergy; mouse; ds; I-Ad; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edwards AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse MHC I-Ad/Ova 323-339 synthetic gene SSCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grammer S,
                                                                                                                                                                                                                                                                                                                                AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
                                                                                                                                                                                                                                                                                                                                           AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
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Chavaillaz P, Jiao JJJ;
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95US-00382454.
97US-00776084.
                                                                                                                                                                                                                                                                                                                                                                                                        ACA60742 standard; DNA; 1385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUN-2003 (first entry)
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01-FEB-1995;
17-JAN-1997;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single chain major histocompatibility complex comprising linked alpha and beta chains - useful for suppressing an immune response to an auto:immune disease. e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
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   GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC 704
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                                                                                                                                                                            Construction; major histocompatibility complex; MHC; fusion complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 66.2%; Score 607.8; DB 2; Length 1385; Best Local Similarity 89.6%; Pred. No. 6.5e-131; Matches 673; Conservative 0; Mismatches 57; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence was used in the construction of major histocompatibility complex (MHC) fusion complexes
                     AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
                                                                                                                                                                                                                                                                                                                                                                            Wong HC;
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                                                                                                                                                                                                                               Location/Qualifiers
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/*tag= a
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                                                                                             BP
                                                                                             AAT86987 standard; DNA; 1385
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                                                                                                                                                                                                                                                                                                                                   96US-00596387
                                                                                                                                                                                        SSC1 single chain gene; ss
                                                                                                                                     (first entry)
                                                                                                                                                          SSC1 single chain gene
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                                                                                                                                                                                                                                                                                                                 30-JAN-1997;
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                                                                                                                                     27-MAR-1998
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Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis, allergies

Fig 27; 126pp; English. Example 17;

The invention relates to a major histocompatibility complex (WHC) fusion complex (I) comprising an MHC molecule that contains a peptide-binding proces, and a presenting peptide covalently (e.g. an antigenic peptide) linked to the MHC molecule, where (I) is capable of modulating the activity of a Tcell. Also included are a DNA construct coding for the complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-As) or human HLA-DR1 (human leukocyte antigen-DR1), a multivalent MHC (fusion complex comprising two or more linked complexes, identifying a peptide that can modulate the activity of T cells (involving introducing into host cells ender conditions using the fost complex and selecting host cells that express MHC fusion complex hat modulate the activity of T cells (involving introducing into host cells ender conditions using be recombinant expression of the complex that modulate the activity of T cells (involving introducing into host complex that modulate the activity of T cells (involving introducing complex that modulate the activity of T cells (involving introducing complex that modulate the activity of T cells (involving introducing complex that modulate the activity of T cells (involving introducing complex that complex MHC protein, a single recombinant expression vector comprising DNA that codes for a T cell costimulatory factor and the alpha and beta chains of the MHC fusion complex. Also included are inducing an immune response in a mammal (including vaccinating a mammal apainst a targeted disorder, by administering DNA sequence comprising a fusion complex, or DNA sequence coding for a fusion complex which is a single chain fusion modulate the agonist and is covalently linked to the MHC protein, or DNA sequence contains a T cell receptor (TCR) antagonist or partial agonist and is covalently linked to the MHC protein, or DNA sequence coding for the fusion complex which is a single chain (including an animal including a peptide chain for including a perinder that can mammal a planting a pep immune response in a mammal. The disorders include an autoimmune disorder such as multiple sclerosis, insulin-dependent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or chronic allergies. The present sequence encodes a mouse MHC class II I-Ad fusion complex of the

Sequence 1385 BP; 316 A; 383 C; 399 G; 287 T; 0 U; 0 Other;

240 360 AGCAGCCCGGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120 164 224 284 09 9 TACGACAGCGACGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACGCCGAG GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCCC 1 ATGGCTCTGCAGATCCCCAGCCTCCTCTCAGCTGCTGTGGTGCTGATGGTGCTG 121 ATCGTGGTGTCCGGCAGCTGGGACGTGGGGGCTCACTAGTGCCCCGAGGCTCTGGA GCTGCTCACGCTGAAATCAACGAAGCTGGTCGTGCTAGCGGAGGGGGGGAAGCGGCGGA GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC GGGACGCAGCGCATACGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC Gaps 21; Length 1385; Indels Score 607.8; DB 8; Pred. No. 6.5e-131; 0; Mismatches 57; Query Match
Best Local Similarity 89.6%;
Matches 673; Conservative ø 61 99 105 181 165 241 225 301

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The present sequence was used in the construction of major

Example 17; Page 137-139; 217pp; English.

900 660 524 584 644 GTCATGCTGGAGATGACCCCTCATCAGGGAGGTCTACACCTGCCATGTGGAGCATCCC 720 704 Single chain major histocompatibility complex comprising linked alpha and beta chains - useful for suppressing an immune response to an auto:immune disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes 345 TACTGGAACAGCCGGAGATCCTGGAGCGAACGCGGGGCCGAGGTGGACACGCCTGC GTGGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGA ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGGCTTGGACCTTCCAGGTCCTG 645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGTCTACACCTGCCATGTGGAGCATCCC AGACACAACTACGAGGGCCGGAGACCAGCACCTCCCTGCGGCGCGCTTGAACAGCCCAAT GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG ACAGTGGGGGTCTCATCCACACACTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG Construction; major histocompatibility complex; MHC; fusion complex; SCT1 single chain gene; ss. 751 705 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735 Wong HC; AGCCTGAAGAGCCCCATCACTGTGGAGTGGA Location/Qualifiers Rhode PR, Jiao J, Burkhardt M, BP AAT86988 standard; DNA; 1508 97WO-US001617. 96US-00596387 (first entry) SCT1 single chain gene. (DADE-) DADE INT INC. WPI; 1997-402555/37. P-PSDB; AAW29213 30-JAN-1997; WO9728191-A1 31-JAN-1996; 27-MAR-1998 07-AUG-1997. Synthetic. 405 585 361 421 481 465 541 AAT86988; mellitus, 525 601 661 721 RESULT 10 Key 셤 ò g g ઠે 셤 ò ò 8 셤 ò g ठ

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complex (sc-MHC) class II complexes that comprise a peptide binding complex (sc-MHC) class II complexes that comprise a peptide binding groove, and a modified class II beta 2 chain or covalently linked crowled class II beta 2 chain or covalently linked complexes immunoglobulin (Ig) light chain constant (CI) region. The MHC complexes are useful for detection and analysis of peptide ligands, pathogenic T cells, for functional, cellular and molecular assays. They can be used to identify and isolate T cell receptor and/or MHC agonists and antagonists. They can be used in vivo to compete with pathogenic antigen presenting cells involved in immune-related disorders. They can also be used to comprishing modified class II beta 2 chains and/or 19-CI regions are soluble and provide enhanced yield. These MHC complexes also can contain single antigenic peptides readily isolated from expressing cells in single cans to detect cells expressing multiple target structures with a single complexe. The present sequence represents a DNA encoding a single chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
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                                                                                                                                                                                                                                                                                                                                                                                    invention relates to new single chain major histocompatibility
                                                                                                                                                                                                                                                                                                                     chain major histocompatibility complex class I complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;
immune-related disorder; antigenic peptide; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                  Wong HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.2%; Score 607.8; DB 2; llarity 89.6%; Pred. No. 6.7e-131; Conservative 0; Mismatches 57;
                                                                                                                                                                                                                                    ם,
                                                                                                                                                                                                                                    Jiao
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                                                                  W09921572-A1
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                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single chain IAd/OVA 323-229 MHC fusion protein encoding DNA.
                                  Sequence 1508 BP; 337 A; 413 C; 441 G; 317 T; 0 U; 0 Other;
                                                                                                   Indels
   histocompatibility complex (MHC) fusion complexes
                                                                Score 607.8; DB 2;
Pred. No. 6.7e-131;
0; Mismatches 57;
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                                                                Query Match
Best Local Similarity 89.6%;
Matches 673; Conservative
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                                                                                                                                                                                                                                                               AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
                                                                                                                                                                                                                                                                                                                                  ACA60743 standard; DNA; 1508 BP
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97US-00776084.
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01-FEB-1995;
17-JAN-1997;
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CC complex (I) comprising an WHC molecule that contains a peptide-binding CC groove, and a presenting peptide covalently (e.g. an antiganic peptide) current and a presenting peptide covalently (e.g. an antiganic peptide) correctly activity of a T cell. Also included are a DNA construct coding for the activity of a T cell. Also included are a DNA construct coding for the CC complex, where the MHC molecule is a class IN MHC (e.g. mouse I-Ad or I-As, or human HLA-DR1 (human laukocyte antigan-DN1), a multivalent MHC tusion complex comprising two or more linked complexes, identifying a cc clusting the host cells cloning vectors that each contain the fusion complex and selecting host cells that expression of the CMHC fusion complex, and selecting host cells that expression of the CMHC fusion complex, and selecting host cells that expression vector complex that modulate the activity of T cells, a single recombinant complex that modulate the activity of T cells, a single recombinant complex that codes for a T cell costimulatory factor and beta chains of the MHC fusion complex. The DNA constructs can contain complex that codes for a T cell costimulatory factor and the alpha and beta chains of the MHC fusion complex. Also included are inducing an immune cresponse in a mammal (including vaccinating a mammal against a targeted disorder, by administering by administering an expression of the fusion complex which is a single chain that on the molecule) and suppressing an immune response in a mammal a DNA sequence comprising an expression vector, encoding a cut mammal a DNA sequence comprising an expression of DNA sequence comprising an expression of the fusion complex which is a single chain to DNA sequence comprising an expression of DNA sequence comprising an expression of DNA sequence comprising a mammal and is a mammal and is contained by a mammal and sequence comprising a peptide that contained an expression of DNA sequence coding for the fusion complex which is a slingle chain to an amount of a mammal against a targete
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Pred. No. 6.7e-131;
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89.6%;
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The invention relates to a major histocompatibility complex (MHC) fusion

Example 17; Fig 28; 126pp; English.

allergies

Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis,

Edwards AC;

Grammer S,

Weidanz JA,

Rhode PR,

Wong HC, Rhodr Chavaillaz P,

Jiao JJJ;

2003-341126/32.

P-PSDB; ABU72107

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GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC 300
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misc_feature
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                                                                                                                                                                                              01-FEB-1995;
                                                                                                       15-FEB-1996.
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6. .1382
6. .1382
6. .86
7.tag= b
7.tag= b
7.label= 1-4d beta chain leader
7.label= "murine MHC class II I-Ad gene beta chain leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHC; major histocompatibility complex; PCR; polymerase chain reaction; T cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myasthenia gravis; ds.
                                      465 GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAAACACTCTGGTCTGTTCG
                CAGGAATGGCCAGGAGGAG
                                                                                                                        525 GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGG
                                                                                                                                                           ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
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/label= I-Ad_alpha2
/note= "murine MHC class II I-Ad gene alpha-2 domain"
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note= "chicken ovalbumin residues 323-339"
138. .167
'*tag= "10 residue linker peptide"
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/note= "24 residue peptide linker"
007. .1067
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| Aabel= I-Ad beta2
| Anote= "muxine MHC class II I-Ad /
| 735. .806
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|label= I-Ad alphal
|note="murine MHC class II I-Ad |
|068. 1352
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|label= I-Ad_betal
|note= "murine MHC class
153. .734
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AAT17588 encodes a murine MHC fusion complex capable of modulating T cell
activity encoded by the vector SCEI. The MHC fusion complex comprises at
least one MHC molecule containing a peptide-binding groove and a
presenting peptide covalently linked to the MHC molecule and opt. a
creamment of the molecule covalently linked to the MHC molecule and opt. a
creamment of the molecule and opt. a
creamment of the molecule and opt. a
creamment of the express the complex. The transformed cells may then
complexed to identify peptides that modulate, pref. antegonise, T cell
activity. DNA encoding a MHC fusion complex or a single chain fusion
complexed may be used to vaccinate a mammal against a targeted disorder.
The fusion complexes may be used to suppress an immune response in an
animal suffering from an immune disorder e.g. multiple sclerosis, insulin
cdependent diabetes mellitus, rheumachoid arthritis, myasthenia gravis or
chronic allergies. The complexes may also be used in the treatment of
chronic allergies. The complexes may also be used in the treatment of
chronic allergies. The complexes may also be used in the treatment of
creation and acts and dogs. The MHC fusion complexes can be
produced such that they contain a single antigenic peptide including one
complexed for T cell interaction
complexed and personed and personed and personed for T cell interaction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Major histocompatability complex fusion complex for modulating T cel activity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
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89.5%; Pred. No. 1.5e-130;
iive 0; Mismatches 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weidanz JA,
                                         /*tag= j
/note= "EE tag"
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95US-00382454
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Matches 672; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DADE-) DADE INT INC.
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P-PSDB; AAR98907.
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Chavaillaz P, Jiao
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note=
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          misc_feature
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TACGACAGCGACGTGGCCGAGTACCGCGCGGTGACCGAGCTCGGGCGGCCGAGACGCCGAG 344
                                                                                                                                                                                        /label= I-Ad_beta_chain_leader
/note= "murine MHC class II I-Ad gene beta chain leader
                                                                                                                                                                                                                                                                                                                                        MHC; major histocompatibility complex; PCR; polymerase chain reaction; T cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myasthenia gravis; ds.
                        AGACACACTACGAGGGGCCCGGAGACCAGCACCTCCCTGCGGCGCCTTGAACAGCCCAAT
                                                        GTCGCCATCTCCCTGTCCAGGACAGAGGCCTCAACCACACAACACTCTGGTCTGTTCG
                                                                                                               GTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGAG
                                                                                                                                                         GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACACTCTGGTCTGTTCG
                                                                                                                                525 GIGACAGATITCIACCCAGCCAAGAICAAAGIGCGCIGGITCAGGAAIGGCCAGGAGAG
                                                                                                                                                                               GTCATGCTGGAGATGACCCCTCATCAGGGAGAGGTCTACACCTGCCATGTGGAGCATCCC
                                                                                                                                               ACAGTGGGGGTCTCATCCACACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG
                TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCCGAGGTGGACACGGCCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= f
/label= I-Ad_beta2
/labe= "murine MHC class II I-Ad gene beta-2 domain"
735. .80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain"
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/label= OVA 323-339
/note= "chicken ovalbumin residues 323-339"
138. .167
/*tag= d
/note= "10 residue linker peptide"
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/labbl= I-Ad_betal
/note= "murine MHC class II I-Ad
453. .734
                                                                                                                                                                                                                         105 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 735
                                                                                                                                                                                                                 AGCCTGAAGAGCCCCATCACTGTGGAGTGGA 751
                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence"
87. .137
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AAT17586 encodes a murine MHC fusion complex capable of modulating T cell
activity encoded by the vector SSC1. The MHC fusion complex comprises at
least one MHC molecule containing a peptide-binding groove and a
presenting peptide covalently linked to the MHC molecule and opt. a
transmembrane domain. DNA encoding a MHC fusion complex may be cloned
into a host cell to express the complex. The transformed cells may then
ce transmembrane domain. DNA encoding a MHC fusion complex may be cloned
activity. DNA encoding a MHC fusion complex or a single chain fusion
conclecule may be used to vaccinate a mammal against a targeted disorder.
The fusion complexes may be used to suppress an immune response in an
animal suffering from an immune disorder e.g. multiple sclerosis, insulin
capendent diabetes mellitus, rheumatoid arthritis, myasthenia gravis or
chronic allergies. The complexes may also be used in the treatment of
through that they contain a single antigenic peptide including one
of known structure, additionally a wide range of peptides can be
controlled for T cell interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AGCAGCCCCGGGACTGAGGCCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC 240
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                                                                                                                                gene alpha-2 domain"
                                                                                                                                                                                                                                                          II I-Ad gene alpha-2 domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edwards AC;
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"24 residue peptide linker"
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Pred. No. 1.5e-130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grammer S,
                                                         /*tag= h
/label= I-Ad alpha1
/note= murine MHC class II
1068. 1352
/*tag= i
/label= I-Ad_alpha2
/note= murine MHC class III
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/note= "6xHis tag"
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95US-00382454
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Best Local Similarity 89.5%;
Matches 672; Conservative (
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/label= I-Ad_beta_chain_leader
/note= "murine MHC class II I-Ad gene beta chain leader
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225 GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC
                                                                                                                                                                          AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGGGGGCTTGAACAGCCCAAT
                                                                             GGGACGCAGCGCATACGGCTCGTGACCAGATACATCTACAACCGGGAGGAGTACGTGCGC
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/label= OVA_323-339
/note= "chicken ovalbumin residues 323-339"
138. 167
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/note= "10 residue linker peptide"
168. .452
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6. .1508
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AAT17587 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SCT1. The MHC fusion complex comprises at least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a cramsmembrane domain. DNA encoding a MHC fusion complex may be cloned into a host cell to express the complex. The transformed cells may then complex or a single chain fusion activity. DNA encoding a MHC fusion complex or a single chain fusion activity. DNA encoding a MHC fusion complex or a single chain fusion complexes may be used to suppress an immune response in an animal suffering from an immune disorder e.g. multiple sclerosis, insulin chaptened mailitus, rheumatoid arthritis, myasthenia gravis or chronic allergies. The complexes may also be used in the treatment of compound such as casts and dogs. The MHC fusion complexes can be confouced such that they contain a single antigenic peptide including one of known structure, additionally a wide range of peptides can be complexed for T cell interaction
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/note= "murine MHC class II I-Ad gene alpha-transmembrane
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/label= I-Ad_alpha1
/note= "murine MHC class II I-Ad gene alpha-2 domain"
1068. 1352
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807. .1067
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95US-00382454
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P-PSDB; AAR98906.
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AGCAGCCCCGGGACTGAGGGCGGAAACTCCATCTGCTTCTCGCCGTCGCTGGAGCACCCG 120
                       AGCAGCCCAAGGAC-------CTTAAGTATCTCTCAGGCTGTTCAC 104
                                     121 ATCGTGGTGTCCGGCAGCTGGAAGGTGGGGGCTCACTAGTGCCCCCGAGGCTCTGGA 180
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Recombinant proteins and molecular complexes derived therefrom, analogus to molecules involved in immune responses
Patent: WO 01019194 A 2 08-FEB-2001;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
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/note="Ligation de fragments d'ADNC"

    921
    note="unnamed protein product"

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AUTHORS
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AR199666 Sequence
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                                                                                                                                                             June 30, 2006, 01:28:47 ; Search time 6493.66 Seconds
                      GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                    - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Kappler, J.W. and Marrack, P.
Product and process for T cell regulation
Parent: US 5820866-A 25 13-OCT-1998;
Location/Qualifiers
1. 489
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Sequence 25 from patent US 5820866.
AR047947.1 GI:5970290
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VAISLERTEALMHHTLVCSVTDFYPAXIKYRWFRNGOEETVGVSSTQLIRNGDWTFO
VLVMLEMTPHQGEVYTCHVEHPSLKSPITVEWRAQSESARSKGGGGSTTAPSAQLKKK
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Oy 121 TyrTrpAsnSerGlnProGluileLeuGluArgThrArgAlaGluValAspThrAlaCys 140	Db 769 AGCACAACTACGAGGGCCGGAGCCCCAGCCCCCTGCGGCGCGCGC	Db 829 ATCGCCATCTCCCTGTCCCAGGACGCCCTCAACCACACACA	Db 889 GrGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCAGGAATGGCCAGGAGGAG 948 Qy 201 ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220	Db 949 ACAGTGGGGGTCTCATCCACAGCTTATTAGGAATGGGGACTGGACCTTCCAGGTCCTG 1008	Oy 221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240	Qy 241 SerLeuLysSerProlleThrValGluTrpArgAlaGlnSerAlaArgSerLys 260	Oy 261GlyGlyGlyGlyGly 264	AR047957 Sequence AR047957	VERSION AR047957.1 GI:5970300 KEYWORDS	SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 1013) AUTHORS Kappler, J. W. and Marrack, P. TITLE Product and process for T cell regulation JUNENAL Patent: US 5920666-A 38 13-OCT-1998;	ë	/organism="unknown" /mol_type="unassigned DNA" ORIGIN	1.44e-111 Length: 1154.00 Matches: 86.8% Conservative:	Best Local Similarity: 84.9% Mismatches: 22 Query Match: 71.2% Indels: 14 DB: 2 Gaps: 4	US-10-048-116B-6 (1-306) x AR047957 (1-1013)	Qy 1 MetAlaLeuGlnIleProSerLeuLeuSerAlaAlaValValValLeuMetValLeu 20	21 SerSerProGlyThrGluGlyGlyAsmSerIleCysPheSerProSerLeuGluHisPro 4	4111eValValSerGlySerTrpAspGlyGlyGlyGlySerLeuVal
	Oy 201 ThrValGlyValSerSerThrGlnLeulleArgAsnGlyAspTrpThrPheGlnValLeu 220	Oy 221 ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240	Qy 241 SerLeuLysSerProlleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260 Db 766 AGCCTGAAGAGCCCCATCACTGGAGTGGAGGGCACAGTCCGAGTCTGCCGGAGCAAG 825	H 3 666	LOCUS AR199666 4724 bp DNA linear PAT 20-APR-2002 DEFINITION Sequence 8 from patent US 6355479. ACCESSION AR199666. VERSION AR199666.1 G1:20249740	S Unknown. ISM Unknown.	Unclassified. Unclassified. AUTHORS Webb,S.R., Wingvist,O., Karlsson,L., Jackson,M.R. and Peterson,P.A. TITLE MHC class II antigen-presenting systems and methods for activating	NAL ES ource		Alignment Scores: Pred. No.: 1.64e-111 Length: 4724 Score: 1161.50 Matches: 228 Percent Similarity: 85.4* Mismatches: 1 Query Match: 2 Gaps: 2 Gaps: 2	US-10-048-116B-6 (1-306) x AR199666 (1-4724)	Oy 1 MetalaLeuGlnIleProSerLeuLeuLeuSerAlaalaValValValValLeuMetValLeu 20 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		IleValValSerGlySerTrpAspGlyGlyGlyGlyGserLeuValProArgGlySerGly) 5. 1.4	538TCCGAAAGGCATTTCGTCGGTCCAGTTCAAGGCCAGTGCTACTACTACTACTACTACTACTACTACTACTACTACTAC	Qy 81 GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 100	Oy 101 TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu 120

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                                                                          TyrapseraspValGlyGluTyrargalaValThrGluLeuGlyargProAspAlaGlu 120
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1 (bases 1 to 1382)

1 hode, P.R., Jiao, J.-A., Burkhardt, M. and Wong, H.C. MHC molecules and uses thereof
Patent: US 6309645-A 123 30-OCT-2001;
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                                                   CysTyrTyrThrAsnGlyThrGlnArglleArgLeuValThrArgTyrIleTyrAsnArg
                                                             GluGluTyrValArgTyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGly
                                                                                                    ValAspThrAlaCysArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArg
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GGTGCACTGGCCAACATTGCTGTCGACAAGGCTGGAGGTGGTGGATCCGGTGGA-----
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3 1 (bases 1 to 1382) . Burkhardt, M. and Wong, H.C. S single chain MHC complexes and uses thereof
AL Patent: US 5869270-A 123 09-FEB-1999;
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Mismatches:
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Conservative:
Mismatches:
Indels:
Gaps:
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 Location/Qualifiers
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                                      AGACACCAACTACGAGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT
                                                                   ValAlaileSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer
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   TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCCGAGGTGGACACGGCGTGC
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Rhode, P.R., Jiao, J.A., Burkhardt, M. and Wol
Single chain MHC complexes and uses thereof
Patent: US 5869270-A 121 09-FEB-1999;
Location/Qualifiers
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/organism="unknown"
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Weldanz, J.A. and wong, H.C.
Phyc complexes and uses thereof
Patent: EP 0991477-A 133 03-MAY-2000;
SUNOL MOLECULAR CORP (US)
                      ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro
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                                 GlyThrGlnArgileArgLeuValThrArgTyrileTyrAsnArgGluGluTyrValArg
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Sequence 123 from Patent EP0997477.
AX032545.1 GI:10279486
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                                                                        Chavaillaz, P.A., Edwards, A.C., Grammer, S., Jiao, J.A., Rhode, P.R. Weidanz, J.A. and Wong, H.C. Mcidanz, J.A. and wong the Complexes and uses thereof Patent: EP 0999/477-A 121 03-MAY-2000; SUNOL MOLECULAR CORP (US)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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121 from Patent EP0997477.

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    /organism="unidentified"
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                                                                                                                  Location/Qualifiers
  AX032543
Sequence 121 from Paten
AX032543
AX032543.1 GI:10279484
                                                           unclassified sequences.
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|GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC
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	ס ַ עט אַס	Alignment Scores: 2.13e-110
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                                                                        GTCGCCATCTCCCTGTCCAGGACACAGCCCCTCAACCACCACAAACACTCTGGTCTGTTCG
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AL Patent: US 6305645-A 122 30-OCT-2001;
Location/Qualifiers
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Matches:
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Mismatches:
Indels:
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Aav12068 Murine IA
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Aat86989 SCE1 sing
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Abj99033 MBP 90-10
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Aad63150 Human maj
Aad62751 Human maj
Adp88246 Lung canc
Adr24869 Breast ca
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Adb57995 Toxicity-
Abt41775 Toxicity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a fusion protein comprising a beta chain of MHC.
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AEC64482
AAD63150
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  -MODEL=frame+ p2n.model - DEV=xlp - Q=/abss/ABSSWEB spool/US10048116/runat_29062006_093309_10102/app_query.fasta_1-Q=/abss/ABSSWEB spool/US10048116/runat_29062006_093309_10102/app_query.fasta_1-DB=N Geneseq_QFWT=fastap-sup_FX=p2n.rng - MINMATCH=0.1 - LOOPECL=0 - LOOPEXT=0-UNITS=bites - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN-0 - ALIGN=15 - MODE=LOCAL-OUTFWT=ptc - NORM=ext - HEAPSIZE=50 - MINLEN=0 - MAXLEN=200000000 - HOST=abss05p - OUTFWT=ptc - NORM=ext - HEAPSIZE=50 - MINLEN=0 - MAXLEN=200000000 - HOST=abss05p - NORM=004 - ANG_SCORES_0 - MAIT - DSPBLOCK=100 - LONGLOG - DEV_TIMEOUT=120 - WGAPPOP=10 - XGAPPRIT=0 - XGAPPRIT=0 - XGAPPRIT=0 - YGAPPRIT=7
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Aat04262 Hybrid IA
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                                                                             June 30, 2006, 01:23:04; Search time 532.723 Seconds (without alignments) 6007.369 Million cell updates/sec
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         GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                     OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                               GGAGGTGGAGGATCCACTACAGCTCCATCAGCTCATGAAAAAAGAAATTGCAAGCACTG
                                                                    ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGluGlu
                                                                                                                       ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu
                                                                                                                                                                          ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= e
/note= "binding site for primer #331 (see AAT04261)"
complement(158. .212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (see AAT04260)"

    16
    /*tag= a
    /note= "probable primer binding site (primer #233)"
    complement (45. .74)

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/note= "primer #333 (see AAT04263) binding site"
371. .389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymerase chain reaction; PCR; primer; amplify; major histocompatability complex; MHC; T-cell receptor; TCR; autoimmune disease; immunodeficiency disease; immune response; immunoproliferation disease; graft-host rejection; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for primer #261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= f
/note= "primer #332_binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
/product= "hybrid IA beta chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= d
/note= "leader region'
complement(119, .172)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
/note= "binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (199. .250)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybrid IA beta chain gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140
                                                                                                                                                                                                                                                                                                                                             from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence encodes a recombinant protein of the invention, comprising a beta chain of MHC molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCCAGGTGGACACGGCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu
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                                                                                                       New soluble recombinant protein, useful e.g. as immunostimulant, comprises dimeric major histocompatibility complex molecule fused immunoglobulin Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 921 BP; 214 A; 265 C; 286 G; 156 T; 0 U; 0 Other;
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Mismatches:
Indels:
Gaps:
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             (CNRS ) CNRS CENT NAT RECH SCI.
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1620.00
100.0%
100.0%
                                       Malherbe
                                                                WPI; 2001-182944/18.
P-PSDB; AAB67481.
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Query Match:
DB:
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I-Ab(beta)-Cholera toxin B subunit-leucine zipper (LZ)-BirA fusion cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGGAGGCTCCGAAAGGCATTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACAAC
                                                                                                                                                  GlyThrGlnArg1leArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg
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              41 IleValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly
                                      ---GAGATCAATGAGGCTGGCAGAGGGGGGGGCTCACTAGTGCCCCGAGGCTCTGGA
                                                                               GlyGlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn
                                                                                                                                                                                     TyrAspSerAspValGluTyrArgAlaValThrGluLeuGlyArgBroAspAlaGlu
                                                                                                                                                                                                                                             TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAACAACACCTCTGGTCTGTTCG
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leucine zipper (LZ)-BirA fusion cDNA"
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1. .945
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Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.
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/*tag= h
note= "probable primer binding site (primer #270)"
311. .825
                                                        /tag= i
/product= "IA beta chain beta 2 region"
521. .550
/*tag= j
/note= "probable primer binding site (primer #271)"
                                                                                                                                                                                                                   /*tag= l
/note= "probable primer binding site (primer #259)"
377. .893
                                                                                                                                                                   *tag= k
note= "probable primer binding site (primer #272)'
                                                                                                                                                                                                                                                                                   note= "probable primer binding site (primer #232)
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Conservative:
Mismatches:
Indels:
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1255.50
95.4%
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Peptide-Class II major histocompatibility complex (MHC) composite, useful for detecting antigen specific CD4+ T-cell, comprises antigen peptide containing epitope of mucous membrane invasive protein, and extracellular
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/product= "I-Ab(beta)-Escherichia coli heat-labile toxin
B subunit (LTB)-leucine zipper (LZ)-BirA fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    class II major histocompatibility complex; MHC; CD4+ T-cell detection; flow cytometry; mucous membrane invasive antigen; I-Ab(beta)-heat-labile toxin B subunit-leucine zipper-BirA fusion; LTB.
                                                                                                                                                                                                                             CTGGTCATGCTGGAGATGACCCCTCGGCGGGGAGAGGTCTACACCTGTCACGTGGAGCAT
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     AsnvalAlaileSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCys
                       SerValThrAspPheTyrProAlaLyslleLysValArgTrpPheArgAsnGlyGlnGlu
                                                                                          TCAGTGACAGATTTCTACCCAGCCAAGATCAAAGTGCGCTGGTTCCGGAATGGCCAGGAG
                                                                                                                                    GluThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnVal
                                                                                                                                                           GAGACGGTGGGGCGTCTCATCCACACACTTATTAGGAATGGGGACTGGACTTCCAGGTC
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                                                                                                                                                                                                                                The invention relates to a novel class II major histocompatibility complex (MHC) antiganic peptide composite comprising a peptide containing the T-cell antiganic determinant of a mucous membrane invasive procein and the extracellular region of a class II MHC molecule or at least part of the extracellular region of the class II MHC molecule having an amino acid sequence comprising one or more deletions, substitutions or microsorganism-derived mivention may be useful for detecting an anticon-specific CD4+ T-cell by flow cytometry and for presenting a microorganism-derived mucous membrane invasive protein as an antigen. The method of the invention nables efficient detection of antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence is that of the class II major histocompatibility complex-related I-cbNA (Alphah)-ChOlecra toxin B subunit (CTB)-leucine zipper (LZ)-BirA fusion compat the invention.
                                                                                                                 Peptide-Class II major histocompatibility complex (MHC) composite, useful for detecting antigen specific CD4+ T-cell, comprises antigen peptide containing epitope of mucous membrane invasive protein, and extracellular
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1235.00
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03-DEC-2002; 2002JP-00351818
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P-PSDB; ADQ31224.
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                                                                                                                                                                        region of MHC
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This nucleotide sequence comprises a PCR product obtained by amplification of mouse splencoyte cDNA using primers (see AAV12065 and AAV12066) designed for the amplification of IAd beta chain full-length cDNA. IAd alpha chain cDNA (see AAV12067) has been similarly obtained. The IAd sequences were cloned into metallothionein promoter (see AAV12062)-driven vector pRmHa-3 prior to sequencing. Major histocompatibility complex (MHC) class II IAd heterodimers were expressed at the cell surface of transfected Drosophila Schneider 2 (ATCC CRL 10974) cells. The invention relates to the preparation and use of synthetic antigen presenting matrices, in particular antigen presenting cells such as insect cells that have been transfected to produce MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Major histocompatibility class II antigen; MHC class II; T cell; T lymphocyte; Th1; Th2; activation; CD4+; antigen presenting cell; APC; autoimmune disease; diabetes; multiple sclerosis; autoimmune thyroiditis; systemic lupus erythromatosus; myasthenia gravis; Crohn's disease; inflammatory bowel disease; allergy; asthma; contact sensitivity; immunotherapy; therapy; IAd beta chain; mouse; ds; circular; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic antigen presenting cell for activating CD4+ T cells - useful treat autoimmune disease, e.g. diabetes, multiple sclerosis, Crohn's disease and inflammatory bowel disease, or allergy, e.g. asthma and
   GAGACGGTGGGGGTCTCATCCACACACTTATTAGGAATGGGGACTGGACCTTCCAGGTC
                                LeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHis
                                                     CTGGTCATGCTGAGAGATGACCCCTCGGGGGGAGGAGGTCTACACCTGTCACGTGGAGCAT
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                                                           The invention relates to a novel class II major histocompatibility complex (MHC) antigenic epetide composite comprising a peptide containing the T-cell antigenic determinant of a mucous membrane invasive protein and the extracellular region of a class II MHC molecule or at least part of the extracellular region of the class II MHC molecule having an amino acid sequence comprising one or more deletions, substitutions or additions. The molecule of the invention may be useful for detecting an antigen-specific CD4+ T-cell by flow cytometry and for presenting a microorganism-derived mucous membrane invasive protein as an antigen-specific activation of CD4+ T-cells in the mucous membrane. The current sequence activation of the class II major histocompatibility complex-related I-the label a coli hear-labile toxin B subunit (LTB)-leucine zipper (LZ)-BirA fusion cDNA of the invention.
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Matches:
Conservative:
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Indels:
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                              Example 3; SEQ ID NO 13; 30pp; Japanese.
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84.9%
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antigen presenting molecules with one or more accessory molecules. The matrices are used to activate naive CD4+ T cells and to shift the ongoing activation state into a preferred differentiated population of Th1 or Th2 cells. Applications include the treatment of autoimmune disease, e.g. diabetes, multiple sclerosis, autoimmune thyroiditis, systemic lupus erythematosus, myssthenia gravis, Crohn's disease and inflammatory bowel disease, or an allergy, e.g. asthma and contact sensitivity
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                                                                                                  Sequence 4724 BP; 1196 A; 1194 C; 1200 G; 1134 T; 0 U; 0 Other;
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228
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Matches:
Conservative:
Mismatches:
Indels:
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1161.50
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85.4%
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/*tags e
/note= "binding site for primer #363 (see AAT04271)"
complement(177. .226)
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'note= "probable primer binding site (primer #270)"
31. .959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= j
note= "probable primer binding site (primer #271)"
44. .568
                                                                                                                                          cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (primer #259)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (primer #272)"
                                                                                                                                                                                                 1. .18
/*tag= a
/note= "probable primer binding site (primer #76)"
complement(40. .74)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= n
/note= "probable primer binding site (primer #59)"
                                                                                                                                                                                                                                                                                                                                                                                        site"
                                                                                                                      Major histocompatability complex; MHC; T-cell receptor; TCR; autoLimune disease; immunodéficiency disease; immune response; immunoproliferation disease; graft-host rejection; therapy; B M12.C3; pM12-IAb-Ea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= m
/note= "probable primer binding site (primer
1000. .1013
                                                                                                                                                                                                                                                                                                                                                                     *tag= g
note= "primer #365 (see AAT04272) binding
85. .403
                                                                                                                                                                                                                                                                                                                                                                                                                                              "IA beta chain beta 2 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site
                                                                                                                                                                                                                                               primer #362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bite
                                                                                                                                                                                                                                                                                                                                                           /note= "primer #364 binding site" complement(212. .266)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY
                                                                                                                                                                                                                                                                          "hybrid IA beta chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "probable primer binding 142. .976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer binding
                                                                                                                                                                                                                                      *tag= b
note= "binding site for
                                                                                                                                                                                                                                                                                   63. .143
/*tag= d
/note= "leader region"
complement(140. .191)
||| ||||||
ATGTTGAGCGGCATCGGGGGC 1149
                                                                                                                                                                                        Location/Qualifiers
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note= "probable
123. .850
                                               BP.
                                               DNA; 1013
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/product= '
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                                                                                   (first entry)
                                                                                                                                                                                                                                                        53. .959
                                                                                                                                                                                                                                                                                                                                                    *tag=
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                                                                                                     IA beta chain
                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAR-1994;
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                                                                                   16-APR-1996
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                                                                                                                                                                      Synthetic
                                                               AAT04269;
                                               AAT04269
                                                                                                      Hybrid
                                    RESULT
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/label= I-Ad_beta_chain_leader
/note= "murine MHC class II I-Ad gene beta chain leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHC; major histocompatibility complex; PCR; polymerase chain reaction; T cell activity modulator; antagonist; immune disorder; allergy; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myasthenia gravis; ds.
                                                                   ThrPheGlnValLeuValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCys
HisValGluHisProSerLeuLysSerProIleThrValGluTrpArgAlaGlnSerGlu
                                                                                                                                                                                                                                                                                         CACGTGGAGCATCCCAGCCTGAAGAGCCCCATCACTGTGGAGTGGAGGGCACAGTCTGAG
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/note= "chicken ovalbumin residues 323-339"
138. .167
/*tag= d
/note= "10 residue linker peptide"
168. .452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "murine MHC class II I-Ad ge
/53. 734
/*tag f
/label= I-Ad beta2
/note= "murine MHC class II I-Ad ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= g
/note= "24 residue peptide linker"
307. .1067
                                                                                                                                                                                                                                                                                                                                                      SeralaArgSerLys-----GlyGlyGlyGly 264
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/label= I-Ad_alpha1
/note= "murine MHC class IJ
1068. 1352
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/label= I-Ad_alpha2
/note= "murine MHC class
1353. .1379
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                                                                                                                                                                                                                                                                   This sequence represents a hybrid IA beta chain gene. This sequence contains a fragment of the IE alpha chain (residues 56-73), as well as a linker and cleavage site. This sequence was transfected into a B cell line (M12.C3) using plasmid planal LAb-Ea. It was found that the encoded sequence was expressed in these cells. Complexes such as this may be used to regulate an immune response. The complexes such as this may be used recognised by a TCR alone or in combination with additional MHC proteins. These complexes are useful for therapeutic purposes and experimental purposes. They can also be used as reagents for the treatment of diseases immunoproliferation diseases, immunodeficiency diseases,
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                                                                                                                                Peptide-MHC complex comprising antigenic peptide, linker and MHC segment - useful as reagents for the treatment of diseases including auto-immune diseases, immuno-stimulatory diseases or graft-host rejection.
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Conservative:
Mismatches:
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                Kappler JW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single chain major histocompatibility complex comprising linked alpha and
beta chains – useful for suppressing an immune response to an auto:immune
                     TyrAspSerkspValGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu
                                                                                            ValThrAspPheTyrProAlaLys1leLysValArgTrpPheArgAsnGlyGlnGluGlu
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                                                                           TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys
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6. .1382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11eValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu
                                                                                                                                                                                                                                                                                                              Major histocompatability complex fusion complex for modulating T celactivity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1382 BP; 320 A; 374 C; 404 G; 284 T; 0 U; 0 Other;
                                                                                                                                                                                                      Grammer S, Edwards AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                         Example 17; Fig 29; 210pp; English.
                                                                                                                                                                                                      Weidanz JA,
                                                                       95WO-US009816
                                                                                                         94US-00283302
95US-00382454
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1145.00
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85.7%
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Query Match:
DB:
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WO9604314-A1
                                                                       31-JUL-1995;
                                                                                                           29-JUL-1994;
                                                                                                                             01-FEB-1995;
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                                                                                                                                                                                                              MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu
                                                                                                                                                                                                                          ATGGCTCTGCAGATCCCCAGCCTCCTCTCAGCTGCTGTGGTGGTGGTGGTGATGGTGGTG
                                                                                                                                                                                                                                                                     41 jieValValSerGjySerTrpAspGjyGjyGjyGjySerLeuValProArgGlySerGjy
                                                                                                                                                                                                                                                                                                                    ATCAACGAAGCTGGTCGTCGTAGCGGAGGGCGGAAGC--------GGCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer
 e.g. multiple sclerosis, rheumatoid arthritis, diabetes
                                                                                 Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;
                                                     major
                                                                                                                                      3 TO
                                                    the construction fusion complexes
                                                     construction
                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                  Length:
Matches:
                              Example 17; Page 140-141; 217pp; English
                                                                                                                                                                                         US-10-048-116B-6 (1-306) x AAT86989 (1-1382)
                                                   The present sequence was used in histocompatibility complex (MHC)
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                                                                                                             1.3e-98
1145.00
87.2%
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The invention relates to a major histocompatibility complex (WHC) fusion complex (I) comprising an MHC molecule that contains a peptide-binding groove, and a presenting peptide covalently (e.g. an antigenic peptide) linked to the MHC molecule, where (I) is capable of modulating the complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-As or human HLA-DR1 (human leukocyte antigen-DR1), a multivalent MHC fusion complex comprising two or more linked complexes, identifying a peptide that can modulate the activity of T cells (involving introducing into host cells cloning vectors that each contain the fusion complex DNA, culturing the host cells under conditions suitable for expression of the MHC fusion complex, and selecting host cells that express MHC fusion complex, and selecting host cells that expression of the C expression vector comprising DNA that codes for the alpha and beta chains of the MHC fusion complex. The DNA constructs can contain beta chains of the fusion complex. Also included are inducing an immune response in a mammal (including vectorating a mammal against a targeted disorder, by administering DNA sequence comprising a fusion complex, or DNA sequence comprising a single chain fusion molecule) and suppressing an immune response in a mammal (including vectoriating a mammal against a targeted disorder, by administering DNA sequence comprising a single chain fusion molecule) and suppressing an immune response in a mammal a DNA sequence comprising a transmembrane domain, and a contain a contain molecule) and suppressing an immune response in a mammal a DNA sequence comprising a transmembrane domain, and a contain a contain and suppressing an immune response in a mammal and suppressing an immune response in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHC; major histocompatibility complex; gene therapy; fusion complex; peptide-binding groove; T cell modulation; olass II MHC; waccine; autoimmune disorder; multiple solerosis; rheumatoid arthritis; insulin-dependent diabetes mellitus; myasthenia gravis; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Edwards AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse MHC I-Ad/Ova 323-339 synthetic gene SCE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chronic allergy; mouse; ds; I-Ad; gene
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95US-00382454.
97US-00776084.
                                                                                                                                                                                                                                 ACA60744 standard; DNA; 1382
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Wong HC, Rhode PR, Wei
Chavaillaz P, Jiao JJJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DADE-) DADE INT INC.
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P-PSDB; ABU72108.
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01-FEB-1995;
17-JAN-1997;
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Synthetic.
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---ACTAGTGGTGGCGGTGGCAGC 755
                                                                                                                                                                                                                                                                                                                                            gene beta chain leader
                                                                                                                                                                                T cell activity modulator; antagonist; PCR; polymerase chain reaction; multiple sclerosis; insulin-dependent diabetes mellitus; rheumatoid arthritis; myasthenia gravis; ds.
                                                                                                                                                                  Vector SSC1-derived single chain gene encoding MHC fusion complex
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/label= OVA_323-339
/note= "chicken ovalbumin residues 323-339"
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note= "24 residue peptide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "10 residue linker peptide
                                                                                                                                                                                                                                                                                                                             /label= I-Ad beta chain leader
/note= "murine MHC class II I-Ad
sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I-Ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= I-Ad beta2
note= "murine MHC class II I-Ad
35. .806
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      705 AGCCTGAAGAGCCCCATCACTGTGGAGTGG----
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/label= I-Ad_alphal
/note= "murine MHC class
1068. 1352
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/note= "murine MHC class
1353. .1382
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                                                                                                DNA; 1385
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95US-00382454
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/*tag= b
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                                                                                                AAT17586 standard;
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01-FEB-1995;
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                                                                                                                                                                                                                                                 Synthetic.
                                                  756
                                                                                                                      AAT17586;
                           261
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                                                                         RESULT 10
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agonist and is covalently linked to the MHC protein, or DNA sequence coding for the fusion complex which is a single chain fusion molecule. The methods are useful for identifying a peptide that can modulate the activity of T cells, inducing an immune response in a mammal (including vaccinating a mammal against a targeted disorder) and for suppressing an immune response in a mammal. The disorders include an autoimmune disorder such as multiple sclerosis, insulin-dependent diabetes mellitus, rhastbring, myastbrenia gravis or chronic allergies. The present sequence encodes a mouse MHC class II I-Ad fusion complex of the
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                                                                                                                              Sequence 1382 BP; 320 A; 373 C; 405 G; 284 T; 0 U; 0 Other;
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Mismatches:
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Single chain major histocompatibility complex comprising linked alpha and beta chains - useful for suppressing an immune response to an auto:immune disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, etc.
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     161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer
                           465 GTCGCCATCTCCCTGTCCAGGACAGAGCCCTCAACCACCACAAAAACACTCTGGTCTGTTCG
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SSC1 single chain gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT17586 encodes a murine MHC fusion complex capable of modulating T cell activity encoded by the vector SSC1. The MHC fusion complex comprises at least one MHC molecule containing a peptide-binding groove and a presenting peptide covalently linked to the MHC molecule and opt. a transmembrane domain. DNA encoding a MHC fusion complex may be cloned into a host cell to express the complex. The transformed cells may then be used to identify peptides that modulate, pref. antegonise, T cell cetivity. DNA encoding a MHC fusion complex or a single chain fusion molecule may be used to vaccinate a mammal against a targeted disorder. The fusion complexes an immune response in an inmal suffering from an immune disorder e.g. multiple sclerosis, insulindependent diabetes mellitus, rheumatoid arthritis, mysathenia gravis or chronic allergies. The complexes and dogs. The MHC fusion complexes can be produced such that they contain a single antigenic peptide including one of known structure, additionally a wide range of peptides can be presented for T cell interaction.
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                                                                                 Major histocompatability complex fusion complex for modulating T cell activity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.
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Chavaillaz P, Jiao J;
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   3 TO 8
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Mismatches:
Indels:
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                                                      US-10-048-116B-6 (1-306) x AAT86987 (1-1385)
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87.2%
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Percent Similarity:
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The invention relates to a major histocompatibility complex (MHC) fusion complex (I) comprising an MHC molecule that contains a peptide-binding groove, and a presenting peptide covalently (e.g. an antigenic peptide) complex (I) comprising an MHC molecule where (I) is capable of modulating the cativity of a T cell. Albo included are a DNA construct coding for the complex, where the MHC molecule is a class II MHC (e.g. mouse I-Ad or I-As or I-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel major histocompatibility complex fusion complex having presenting peptide covalently linked to MHC molecule containing peptide-binding groove, used for suppressing immune response in multiple sclerosis,
MHC; major histocompatibility complex; gene therapy; fusion comple. peptide-binding groove; T cell modulation; class II MHC; vaccine; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes mellitus; myasthenia gravis; immunogen; chronic allergy; mouse; ds; I-Ad; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edwards AC;
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97US-00776084
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Chavaillaz P, Jiao JJJ;
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P-PSDB; ABU72106.
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17-JAN-1997;
                                                                                                                                                                                                                                       26-DEC-2002
                                                                                                                                                   Synthetic.
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287 T; 0 U; 0 Other;

C; 399 G;

Sequence 1385 BP; 316 A; 383

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gene alpha-transmembrane
                                                                                                                                                                              chain_leader
class II I-Ad gene beta chain leader
                                   MHC; major histocompatibility complex; PCR; polymerase chain reaction; 
I cell activity modulator; antagonist; immune disorder; allergy; 
multiple sclerosis; insulin-dependent diabetes mellitus; 
rheumatoid arthritis; myasthenia gravis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene alpha-2 domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Major histocompatability complex fusion complex for modulating T cell activity - used in the treatment of immune disorders, e.g. multiple sclerosis, IDDM and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                   note= "murine MHC class II I-Ad gene beta-1 domain"
53. .734
                                                                                                                                                                                                                                                                                                                                                                                   domain"
               SCT1-derived single chain gene encoding MHC fusion complex.
                                                                                                                                                                                                                                                                                                                                                                                  gene beta-2
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/label= OVA 323-339
/note= "chicken ovalbumin residues 323-339"
138. 167
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note= "24 residue peptide linker"
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/note= "10 residue linker peptide"
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/label= I-Ad_alpha2
/note= "murine MHC class II I-Ad
1353. .1505
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/label= I-Ad_beta2
/note= "murine MHC class II I-Ad
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/note= "murine MHC class II I-Ad
1068. .1352
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//abba= I-Ad_alpha-TM
//note= "murine MHC class II I-Ad
domain"
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6. .1508
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'note= "murine MHC
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'label= I-Ad_betal
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95US-00382454.
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Chavaillaz P, Jiao J;
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01-FEB-1995;
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                                                                                              Synthetic
               Vector
   66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA---- 119
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           1385
227
4
24
10
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            Length:
Matches:
Conservative:
Mismatches:
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activity encodes a murine MHC fusion complex capable of modulating T cell
activity encoded by the vector SCT1. The MHC fusion complex comprises at
least one MHC molecule containing a peptide-binding groove and a
c presenting peptide covalently linked to the MHC molecule and opt. a
c transmembrane domain. DNA encoding a MHC fusion complex may be cloned
into a host cell to express the complex. The transformed cells may then
be used to identify peptides that modulate, pref. antegonies, T cell
activity. DNA encoding a MHC fusion complex or a single chain fusion
molecule may be used to vaccinate a mammal against a targeted disorder.
The fusion complexes may be used to suppress an immune response in an
c animal suffering from an immune disorder e.g. multiple sclerosis, insulin
dependent diabetes mellitus, rheumacoid arthritis, myasthenia gravis or
chronic allergies. The complexes may also be used in the treatment of
livestock and pets such as casts and dogs. The MHC fusion complexes can be
produced such that they contain a single range of peptides can be
coppendented for T cell interaction
copperated and pet such as casts and dogs. The MHC fusion complexes can be
copperated for T cell interaction
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                                                 Single chain major histocompatibility complex comprising linked alpha and beta chains - useful for suppressing an immune response to an auto:immune disease, e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, etc.
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          645 GTCATGCTGGAGATGACCCCTCATCAGGGAGAGTCTACACCTGCCATGTGGAGGCATCCC
                                      SerLeuLysSerProlleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major histocompatibility complex; MHC; fusion complex;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence was used in the construction of major histocompatibility complex (MHC) fusion complexes
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Best Local Similarity:
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                                                               GlyGlyGlySerGluArgHisPheValValGlnPheLygGlyGluCysTyrTyrThrAsn
                                                                             TACGACAGGACGTGGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCCGCCAGACGCCGGG
                                                                                                                                                                        TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys
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SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro
               66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA----
                                                                                                    GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg
                                                                                                                                      TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu
                                                                                                                                                                                    TACTGGAACAGCCAGCCGGAGATCCTGGAGCGAACGCGGGCCCGAGGTGGACACGGGCGTGC
                                                                                                                                                                                                           ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn
                                                                                                                                                                                                                      GTCGCCATCTCCCTGTCCAGGACAGGCCCTCAACCACCACACACTCTGGTCTCG
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                                ileValValSerGlySerTrpAspGlyGlyGlyGlySerLeuValProArgGlySerGly
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immune-related disorder; antigenic peptide; fusion protein; ss.
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The invention relates to new single chain major histocompatibility complex (sc-MHC) class II complexes that comprise a peptide binding groove, and a modified class II beta 2 chain or covalantly linked cimmunoglobulin (Ig) light chain constant (CI) region. The MHC complexes are useful for detection and analysis of peptide ligands, pathogenic T-cells, for functional, cellular and molecular assays. They can be used to identify and isolate T cell receptor and/or MHC agonists and antagonists. They can be used in vivo to compete with pathogenic antigen presenting cells involved in immune-related disorders. They can also be used to raise antibodies and to screen immune cells. It is also use in a method of suppressing an immune response in mammals. The sc-MHC complexes comprising modified class II beta 2 chains and/or Ig-CI regions are soluble and provide enhanced yield. These MHC complexes also can contain single antigent quantities. The polyspecific MHC complexes also provide a means to detect cells expressing multiple target structures with a single complex. The present sequence represents a DNA encoding a single chain
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ArgHisasnTyrGluGlyProGluThrSerThrSerLeuargargLeuGluGlnProasn 160 	ValalaileSerLeuSerArgThrGlualaLeuAsnHisHisHsasnThrLeuValCysSer 180 	ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu 200 	ThrvalglyvalserserThrGlnLeulleArgAanGlyAapTrpThrPheGlnValLeu 220 	ValMetLeudlumetThrProHisclnGlyGluValTyrThrCysHisValCluHisPro 240 	SerleulyeSerprolleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260 	Glyser 265 GGTTCC 770
ArghibasnTyrGlugi 	ValAlaIleSerLeuS(ValThrAspPheTyrP 	ThrvalGlyvalSerSerser	ValMetLeuGluMetT 	SerLeuLysSerProl.	GlyGlyGlyGlySer
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Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses
Patent: WO 1019194-A 2 08-FEB-2001;
CENTRE NATIONAL DE LA RECHRECHE SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xrefe"taxon:32630"
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4520.078 Million cell updates/sec
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               GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                      - nucleic search, using frame_plus_p2n model
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GSWDGGGSLVPRGSGGGGSERHFVVQFKGECYYTNGTQRIRLVTRYIYNREEYVRYD
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VAI SLSRTEALNHHNTLVGSVTDFYPAKIKVRWFRNGQEETVGVSSTQLIRNGDWTFQ
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29-SEP-1999 225 285 100 120 405 140 160 9 80 61 ATGGCTCTGCAGATCCCCCAGCCTCCTCTCAGCTGCTGGTGGTGGTGGTGGTGGTGCTG TyrAspSerAspValGlyGluTyrArgAlaValThrGluLeuGlyArgProAspAlaGlu ---GAGATCAATGAGGCTGGCAGAGGTGGGGGGTCACTAGTGCCCCGAGGCTCTGGA GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrThrAsn 226 GGTGGAGGCTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGGAGTGCTACTACACCCAAC GlyThrGlnArgIleArgLeuValThrArgTyrIleTyrAsnArgGluGluTyrValArg 346 TACGACAGCGACGTGGGCGAGTACCGCGCGGTGACCGAGCTGGGGCGGCCAGACCCGAG TyrTrpAsnSerGlnProGluIleLeuGluArgThrArgAlaGluValAspThrAlaCys ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn 466 AGACACAACTACGAGGGCCGGAGACCAGCACCTCCCTGCGGGGGGGTTGAACAGCCCAAT SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisHisAsnThrLeuValCysSer MetAlaLeuGlnIleProSerLeuLeuLeuSerAlaAlaValValValLeuMetValLeu PAT 893 242 7 5 M Unknown.
Unclassified.
B 1 (bases 1 to 893)
KS Rappler,J.W. and Marxack,P.
Product and process for T cell regulation
Product: US 5820866-A 25 13-OCT-1998;
Location/Qualifiers
893 US-10-048-116B-6_COPY_1_300 (1-300) x AR047947 (1-893) Length:
Matches:
Conservative:
Mismatches:
Indels: DNA

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1128
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                                                                                         ArgHisAsnTyrGluGlyProGluThrSerThrSerThrSerDeuArgLeuGluGlnGlnProAsn
                                                                769 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT
                                                    161 ValAlaIleSerLeuSerArgThrGluAlaLeuAsnHisAsnThrLeuValCysSer
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                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 1013)

Rappler, J.W. and Marrack, P.
Product and process for T cell regulation
Patent: US 5820866-A 38 13-OCT-1998;
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Matches:
Conservative:
Mismatches:
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Sequence 38 from patent US 5820866.
AR047957.1 GI:5970300
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/organism="unknown"
/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                      Unclassified.

1 (bases 1 to 4724)

1 (bases 1 to 4724)

Webb,S.R., Wingvist,O., Karlsson,L., Jackson,M.R. and Peterson,P.A.
Webb,S.R. II antigen-presenting systems and methods for activating CD4+ T cells
Patent: US 6355479-A 8 12-MAR-2002;

Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 8 from patent US 6355479,
AR199666 GI:20249740
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Query Match:
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66 AGCAGCCCAAGGACCTTAAGTATCTCTCAGGCTGTTCACGCTGCTCACGCTGAA-----
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Rhode, P.R., Jiao, J.-A., Burkhardt, M.
MHC molecules and uses thereof
Patent: US 6309645-A 123 30-OCT-2001;
Location/Qualifiers
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Sequence 123 from patent US 6309645.
AR175097
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/mol_type="unassigned DNA"
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Rhode, P.R., Jiao, J.-A., Burkhardt, M. and Wong, H.C. Single chain MMC complexes and uses thereof Patent: US 5869270-A 123 09-FEB-1999;
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Patent: Ep 1526141-A 123 27-APR-2005;
Altor BioScience Corporation (US)
Location/Qualifiers

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                      ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro
 105 AGACACAACTACGAGGGGCCGGAGACCAGCACCTCCCTGCGGCGGCTTGAACAGCCCAAT
                                                                     ValThrAspPheTyrProAlaLysIleLysValArgTrpPheArgAsnGlyGlnGluGlu
                                                                                   ThrValGlyValSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu
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Unclassified.
1 (bases 1 to 1385)
1 Khode, P.R., Jiao, J.-A., Burkhardt, M. and Wor
Single chain MHC complexes and uses thereof
Patent: US 5869270-A 121 09-FEB-1999;
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Matches:
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AR033962
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1. .1385
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Who complexes and uses thereof
Patent: EP 0997477-A 133 03-MAY-2000;
SUNOL MOLECULAR CORP (US)
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                      GTCATGCTGGAGATGACCCCTCATCAGGAGAGGTCTACACCTGCCATGTGGAGCATCCC
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Matches:
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Sequence 123 from Patent EP0997477.
AX032545.
AX032545.1 GI:10279486
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MHC complexes and uses thereof
Patent: EP 1526141-A 121 27-APR-2005;
Altor BioScience Corporation (US)
Location/Qualifiers
1. 1385
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Sequence 121 from Patent EP1526141.
CS079299.1 GI:63093741
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Rhode, P.R., Jiao, J.-A., Burkhardt, M. and IMC molecules and uses thereof
Patent: US 6309645-A 121 30-OCT-2001,
Location/Qualifiers
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Sequence 121 from patent US 6309645.
AR175095.
AR175095.1 GI:17916394
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                                               Jiao, J.A., Rhode, P.R.,
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Mismatches:
Indels:
                                             Chavaillaz, P.A., Edwards, A.C., Gramme Weidanz, J.A. and Wong, H.C. Mhc complexes and uses thereof Patent: EP 0997477-A 121 03-MAY-2000; SUNOL MOLECULAR CORP (US)
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Matches:
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GGGGGAAACTCCGAAAGGCATTTCGTGGTCCAGTTCAAGGGCGAGTGCTACTACACCAAC
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Sequence 121 from Patent EP0997477.
AX0332643.1 GI:10279484
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E 1 (bases 1 to 1508)
S Rhode, P. R., Acevedo, J., Burkhardt, M., Jiao, J.-a. and Soluble WHC complexes and methods of use thereof
AL Patent: US 6232445-A 24 15-MAY-2001;
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/mol_type="unassigned DNA"
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Rhode, P.R., Jiao, J.-A., Burkhardt, M. and Wong, H.C. Single chain MHC complexes and uses thereof Patent: US 5869270-A 122 09-FEB-1999;
Location/Qualifiers
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/organism="unknown"
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Mismatches:
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                       GlyGlyGlySerGluArgHisPheValValGlnPheLysGlyGluCysTyrTyrThrAsn
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                                                                                                                                                ValThrAspPheTyrProAlaLyslleLysValArgTrpPheArgAsnGlyGlnGluGlu 200
                                   160
                                                                                                                                                                                      ThrvalGlyvalSerSerThrGlnLeuIleArgAsnGlyAspTrpThrPheGlnValLeu 220
                                                                                                                                                                                                                          ValMetLeuGluMetThrProHisGlnGlyGluValTyrThrCysHisValGluHisPro 240
                                                                                  Val Alaile SerLeu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser 180
                                                                                                                               524
                                                                                                                                                                                                         644
                                                                                                                                                                                                                                     SerLeuLysSerProlleThrValGluTrpArgAlaGlnSerGluSerAlaArgSerLys 260
                                                                                                                                                                                                                                                                                  AGCCTGAAGAGCCCCATCACTGTGGAGTGG-----ACTAGTGGTGGCGGTGGCAGC 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerSerProGlyThrGluGlyGlyAsnSerIleCysPheSerProSerLeuGluHisPro 40
ArgHisAsnTyrGluGlyProGluThrSerThrSerLeuArgArgLeuGluGlnProAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGCCATCTCCCTGTCCAGGACAGAGGCCCTCAACCACCACAAACACTCTGGTCTGTTCG
                                                                                                                                                                                                 Winknown.

Unclassified.

E 1 (bases 1 to 1508)

S Rhode, P.R., Jiao, J.-A., Burkhardt, M. and Wong, H.C.

ML molecules and uses thereof

AL Patent: US 630845-A 122 30-OCT-2001;

Location/Qualifiers

1. 1508

/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                           linear
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Matches:
Conservative:
Mismatches:
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Sequence 122 from patent US 6309645.
AR175096.1 GI:17916395
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1145.00
87.2%
85.7%
72.8%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                       Unknown.
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Pred. No.:
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ACCESSION
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KEYWORDS
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DB:
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AUTHORS
TITLE
JOURNAL
FEATURES
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